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Patentanmeldung Nr. Patent application No. Demande de brevet n°

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Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
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R C van Dijk

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Chlamydia pneumoniae antigens

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The present invention relates to isolated nucleic acid molecules, which encode antigens for *Chlamydia pneumoniae*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Chlamydia pneumoniae.*

Chlamydia pneumoniae is an obligate intracellular bacterium and recognized as a significant human pathogen. It is a common cause of pneumoniae and upper respiratory tract disease in both, hospital and outpatient settings, accounting for approximately 7 to 10% of cases of community-aquired pneumoniae among adults {Montigiani, S. et al., 2002}. Infection with *Chlamydia pneumoniae* has also been associated with other respiratory tract diseases such as bronchitis, sinusitis, asthmatic bronchitis, adult-onset asthma, and chronic obstructive pulmonary disease {Murdin, A. et al., 2000}. Importantly, *Chlamydia pneumoniae* infection has also been associated with atherosclerosis and cardiovascular disease, which was indicated for example by seroepidemiologic studies or detection of *C. pneumoniae* in atherosclerotic plaques {Montigiani, S. et al., 2002}.
It was recently suggested that the Gram-negative Chlamydiaceae, a family of uncertain origin and the only members of the order Chlamydiales, can been divided into two genera, *Chlamydia* and *Chlamydophila*, by 16S rRNA phylogeny {Everett, K. et al., 1999}. According to this suggestion, three species are described within the genus *Chlamydia*: *Chlamydia trachomatis*, *Chlamydia muridarum* and *Chlamydia suis*. The species *Chlamydia psittaci, pecorum* and *pneumoniae* were suggested to be renamed to *Chlamydophila psittaci, pecorum* and *pneumoniae*. Nevertheless, bacteria of both genera share biological and biochemical properties. For the present invention, the newly suggested nomenclature has not been used yet, but for reasons of completeness it should be mentioned that the species *Chlamydia pneumoniae* and *Chlamydophila pneumoniae* are identical.
Sequencing of seven Chlamydiaceae genomes from four different species, has demonstrated that profound differences in host range and disease can be caused by fairly subtle variations in gene content {Read, T. et al., 2003}. The Chlamydiaceae are classified among the eubacteria as a well-isolated group, with only a very weak link to the planctomyces. The Chlamydiaceae therefore exhibit some unique characteristics within the eubacteria, in particular their development cycle and the structure of their membranes. They have a unique two-phase cell cycle: the elementary body, a small extracellular form, which attaches to the host and is phagocytosed. Subsequently, it is converted in the phagosome to the replicative intracellular form, the reticulate body. As obligate intracellular bacteria, the Chlamydiaceae multiply in eukaryotic cells at the expense of their energy reserves and nucleotide pools; they are responsible for a wide variety of diseases in mammals and birds.

The species *Chlamydia trachomatis* is the best characterized. Besides a murine strain, it is divided into two groups which are distinguishable by the nature of the diseases for which they are responsible: trachoma, genital attack and venereal lymphogranulomatosis. There are fifteen human serotypes of *Chlamydia trachomatis* (A, K) and LGV (L1, L2, L3). Strains A to C are mainly found in eye infections, whereas strains D to K and LGV are essentially responsible for genital entry infections. It should be mentioned that the LGV strains are responsible for systemic diseases. Historically, the characterization of the *Chlamydia trachomatis* microorganism was only successfully carried out in 1957, after a series of isolations in cell cultures.

The species *Chlamydia psittaci* infects many animals, in particular birds, and is transmissible to humans. It is responsible for atypical pneumonia, for hepatic and renal dysfunction, for endocarditis and for conjunctivitis.

Chlamydia pecorum does not infect humans, but is rather a pathogen of ruminants.

It was in 1983 that *Chlamydia pneumoniae* was recognized as a human pathogen {Grayston, J. et al., 1986}. Thereafter, special attention has been paid to this bacterium and it is estimated {Gaydos, C. et al., 1994} that 10% of pneumonias, and 5% of bronchitides and sinusites are attributable to *Chlamydia pneumoniae* {Aldous, M. et al., 1992}. More recently, the association of this bacterium with the pathogenesis of

asthmatic disease and of cardiovascular impairments is increasingly of interest.

Serological studies have shown that *Chlamydia pneumoniae* infection is common in children between 5 ar 16 years of age. Before this age, it is rare to find antibodies and the best available data indicate th children begin to seroconvert at an age of about 5 years. The increase in the number of individua carrying antibodies correlates then with age up to 20 years. Accordingly, 50% to 70% of adults are carrie of antibodies. Since the persistence of induced antibodies over time is limited to 3 or at most 5 years aft a first infection, it is suggestive that frequent reinfection occurs during the entire lifespan. The annu seroconversion rate is about 6 to 8% between 8 and 16 years {Kuo, C. et al., 1995} and the seroprevalen of the disease before the age of 15 years is identical between both sexes. After this age, men are mo frequently infected than women in all regions worldwide.

These Chlamydia infections are geographically highly widespread throughout the world {Tong, C. et a 1993}, with the lowest infection rates observed in developed countries of the north such as Canada a the Scandinavian countries. In contrast, the highest prevalence rates are found in the less develop countries of tropical regions where the infection may occur before the age of 5 years. Humans are t only known reservoir for *Chlamydia pneumoniae* and it is probable that the infection is caused by perso to-person transmission by respiratory secretions {Aldous, M. et al., 1992}. The chain of transmission m also appear to be indirect {Kleemola, M. et al., 1988}, suggestive of an infection caused by an effecti transmission and of the possibility that also asymptomatic carriers exist, which could be an explanati of the high prevalence of the disease. This is also in accordance with the finding that *Chlamy pneumoniae* can survive for up to 30 hours in a hostile environment {Falsey, A. et al., 1993}, although infectivity of the microorganism in the open air decreases rapidly under conditions of high relat humidity. The period of incubation is with several weeks significantly longer than that of many ot respiratory pathogenic bacteria.

The main clinical manifestations caused by *Chlamydia pneumoniae* are essentially respiratory diseas Pneumonia and bronchitis are the most frequent, because they are clinically obvious and the infectio agent may be identified. Isolation of the etiologic agent is difficult though and paired acute- a convalescent-phase sera are required to confirm the diagnosis using antibody tests. The asymptoma diseases caused by *Chlamydia pneumoniae* are probably numerous (e.g. {Grayston, J., 1992}). Ot syndromes such as sinusitis, purulent otitis media {Ogawa, H. et al., 1992}, or pharyngitis have b described, as well as infections with respiratory impairments similar to asthma {Hahn, D. et al., 19 *Chlamydia pneumoniae* has also been associated with sarcoidosis, with erythema nodosum {Sundelof, B al., 1993} and one case of Guillain-Barre syndrome has been described {Haidl, S. et al., 1992}. involvement of *Chlamydia pneumoniae* in Reiter's syndrome has also been evaluated {Braun, J. et al., 199

Cardiovascular diseases are the major cause of death in thecountries of the Western world. association of *Chlamydia pneumoniae* with the development of cardiovascular diseases such as coron heart disease and myocardial infarction was first suspected due to the observation of high antibody le in of patients with heart disease (e.g. {Shor, A. et al., 1992}). In addition, anatomicopathological microbiological studies were able to detect in the vessels. Studies from several countries have also sho that *Chlamydia pneumoniae* infection correlates with with atheromatous impairments in patients {Grayston, J., 1996}). Thus it also appears that the bacterium is more frequently found in atheromatous lesions, than in early lesions, but that it is not found in subjects free of atheroma disease. It is therefore supported by these studies that the atheroma plaque is very strongly correl with the presence of *Chlamydia pneumoniae*. Nevertheless, the role that the bacterium plays in vasc pathology is not yet defined.

For the treatment of *Chlamydia pneumoniae* infections, there are only limited data available from contro ~~clinical studies. Similar to Lymes disease and mycoplasma infection, and due to the intracellular natu~~ *C. pneumoniae*, long term antimicrobial treatment is needed. This extensive antimicrobial treatme

required for eradication of *C. pneumoniae* from macrophages and endothelial cells of infected arteries. Unlike penicillin, ampicillin or the sulphamides, antibiotics such as erythromycin, tetracycline, doxycycline, ofloxacin, clinafloxacin, ciprofloxacin, azithromycin, clindamycin, and minocycline show an antibiotic activity in vitro against *Chlamydia pneumoniae*. However, any treatment at high doses should be continued for several weeks in order to avoid a recurrence of the infection. Accordingly, the use of two new macrolides, clarithromycin and azithromycin, whose diffusion, bioavailability and half-life allow shorter and better tolerated cures, is nowadays preferred. Unfortunately, many conventional treatments against Chlamydia still fail, resulting in a significant rate of recurrence and morbidity. In the absence of definitive proof based on the results of clinical studies, an effective, without recurrences, and well-tolerated treatment of *Chlamydia pneumoniae* infections therefore remains desirable.

A very important issue is the development of a specific and sensitive diagnosis, which can be carried out conveniently and rapidly, allowing early screening for the infection. Unfortunately, methods based on *Chlamydia pneumoniae* culture are slow and require a considerable know-how because of the difficulty involved in the collection, preservation and storage of the strain under appropriate conditions. On the other hand, methods based on antigen detection (EIA, DFA) or on nucleic acid amplification (PCR) provide tests, which are more suitable for laboratory practice. A reliable, sensitive and convenient test, which allows distinction between serogroups and a fortiori between *Chlamydia pneumoniae* species is highly desirable. This is all the more important, because the symptoms of *Chlamydia pneumoniae* infection appear slowly, and because not all of the pathologies associated with these infections have yet been identified. In addition, an association is suspected between these infections and serious chronic infections, asthma or atherosclerosis. Although sensitive and specific tests based on antigen detection have been developed, there remains a need for standardized PCR based detection protocols and tests {Dowell, S. et al., 2001}.

Chlamydial infections are often chronic and recurrent, suggesting that protective immunity against Chlamydia is weak and not necessarily bactericidal or sterilizing. There are currently no available vaccines against chlamydial infections. Although the number of studies and of animal models developed is high, the antigens used have not induced sufficient protective immunity to lead to the development of human vaccines.

A more detailed understanding of the biology of *Chlamydia pneumoniae*, the interactions of the bacteria with their hosts, their escape from immune defenses of the host in particular, but also their involvement in the development of the associated pathologies, will allow a better control, treatment or prevention of Chlamydia caused diseases. It is therefore essential, to use novel molecular tools, which allow to develop new preventive and therapeutic treatments, new diagnostic methods and new vaccine strategies which are specific, effective and tolerated.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic function and genetic background, *Chlamydia pneumoniae* is very distinctive from *Staphylococcus* strains. Importantly, the selection of sera for the identification of antigens from *C. pneumoniae* is different from that applied to the *S. aureus* screens. Infections with *Chlamydia pneumoniae* are detected and diagnosed by serology, since the pathogen is not culturable with routine microbiological methods. We have selected patients' sera having high titer against *C. pneumoniae* detected by a standard Chlamydia ELISA kit routinely used in the clinic for diagnosis of acute, chronic and persistent infections caused by Chlamydia species. Our selection mainly relied on the presence of high affinity IgG antibodies, allowing the identification of patients in convalescent phase. The pre-selected sera having the highest titers were subsequently analysed by immunoblotting to ensure antibody reactivities against multiple proteinaceous antigens present in *C. pneumoniae*. This approach for selection of human sera is basically very different

from that used for *S. aureus*, where carriage or even disease cannot be always associated with hi[illegible] antibody levels.

The genomes of the two bacterial species *C. pneumoniae* and *S. aureus* by itself show a number [illegible] important differences. While the genome of *S. aureus* harbours 2.85 Mb, the genome of *C. pneumon*[illegible] contains app. 1.23 Mb, less than half of the size of *S. aureus* and many other bacterial genomes. They ha[illegible] an average GC content of 33 and 40.6%, respectively and only 586 of the *S. aureus* genes have a mat[illegible] with a gene in *C. pneumoniae* with at least 40% identity on the amino acid level. This means that of t[illegible] 1073 genes of *C. pneumoniae* less than 55% have a homologous sequence in *S. aureus*. In addition, the t[illegible] bacterial species require not only different growth conditions and media for propagation, but [illegible] pneumoniae is an obligate intracellular pathogen, while *S. aureus* mainly lives extracellular[illegible] Furthermore, *C. pneumoniae* is a strictly human pathogen, but *S. aureus* can also be found infecting a ra[illegible] of warm-blooded animals. A list of the most important diseases, which can be inflicted by the t[illegible] pathogens is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impeti[illegible] folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumo[illegible] osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *C. pneumoniae* causes mai[illegible] pneumoniae and upper respiratory tract disease.

The complete genome sequence of a several isolates of *C. pneumoniae*, was determined by vari[illegible] institutions {Kalman, S. et al., 1999}; {Read, T. et al., 2000}; {Shirai, M. et al., 2000}; see [illegible] http://www.tigr.org/tigr-scripts/CMR2/CMRHomePage.spl). Although the two strains AR39 and CWL[illegible] were isolated in the U.S.A. before 1987 and Japan in 1994, respectively, their sequence is to a high deg[illegible] identical, indicating a divergence in recent human history. In addition to these three *C. pneumo*[illegible] strains, the sequence of two *C. trachomatis* strains {Kalman, S. et al., 1999}; {Read, T. et al., 2000} and tha[illegible] *C. psittaci* {Read, T. et al., 2003} have been determined.

The problem underlying the present invention was to provide means for the development[illegible] medicaments such as vaccines against *C. pneumoniae* infection. More particularly, the problem wa[illegible] provide an efficient, relevant and comprehensive set of nucleic acid molecules or hyperimmune se[illegible] reactive antigens from *C. pneumoniae* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimm[illegible] serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected f[illegible] the group consisting of:

a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule sele[illegible] from Seq ID No 31-60.
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule [illegible] or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nu[illegible] acid molecule of a), b), or c)
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise t[illegible] nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least [illegible] preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimm[illegible] serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the g[illegible] consisting of

a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule sel[illegible]

from Seq ID No 5, 7-8, 14-16, 18-22, 24-27, 29-30.

b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a C. *pneumoniae* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 91-120.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 65, 67-68, 74-76, 78-82, 84-87, 89-90.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", "Predicted class II restricted T-Cell epitopes / regions" "Predicted class I restricted T-Cell epitopes / regions", and "location of identified immunogenic region" of Table 1; the serum reactive peptide epitopes of Table 2, especially peptides comprising amino acids 18-29, 60-78, 89-95, 100-105, 124-143, 166-180, 187-194, 196-208, 224-242, 285-294, 305-311, 313-320, 351-360, 368-373, 390-403, 411-429, 432-470, 483-489, 513-523, 535-543, 548-564, 579-587, 589-598, 604-612, 622-627, 632-648, 55-84, 190-207, 323-331, 370-390, 551-570, 606-614, 633-647, 39-129, 224-296 and 464-609 of Seq ID No 61; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 60, 63, 67, 70, 126, 129, 133, 136, 169, 186, 200, 308, 371, 414, 421, 434, 444, 459, 503, 512, 532, 540, 547, 601, 625, 632, 634, 637, 99, 529, 25, 38, 59, 155, 278, 285, 412, 420, 441, 451, 457, 481, 506, 510, 524, 536, 539, 554, 578, 596, 638, 179 and 604 of Seq ID No 61; 4-29, 31-38, 46-64, 66-80, 109-115, 131-139, 152-160, 170-183, 198-234, 239-255, 267-290, 301-313, 318-324, 336-345, 350-365, 380-386, 65-82, 123-165, 268-290, 299-307, 320-329, 336-347, 76-103, 226-239 and 267-333 of Seq ID No 62; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 4, 13, 69, 93, 149, 174, 273, 277, 298, 305, 312, 319, 375, 28, 303, 3, 58, 73, 100, 153, 191, 223, 227, 232, 251, 269, 286, 343, 374 and 238 of Seq ID No 62; 20-33, 35-43, 47-60, 77-92, 113-124, 137-145, 185-196, 66-75 and 92-214 of Seq ID No 63; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length

starting from the position of: 32, 48, 49, 113, 77, 118, 139, 185, 2, 24 and 120 of Seq ID No 63; 47-64, 13 155, 157-167, 182-198, 212-233, 247-259, 291-303, 315-337, 345-350, 355-368, 373-379, 58-72, 183-196, 249-26 315-323, 334-342, 347-356, 358-366 and 6-188 of Seq ID No 64; and fragments with at least 6 amino ac length, preferably at least 9 amino acid length starting from the position of: 135, 160, 183, 184, 204, 24 256, 293, 296, 318, 319, 356, 372, 94, 13, 60, 159, 163, 189, 204, 220, 233, 300, 333, 335, 356, 362, 198 and 2 of Seq ID No 64; 4-36, 43-49, 60-75, 96-107, 113-123, 132-172, 186-193, 217-229, 231-250, 260-282, 284-29 298-312, 315-330, 5-38, 67-77, 113-127, 134-145, 147-156, 220-236, 271-283, 285-293, 296-304, 309-321 a 159-217 of Seq ID No 65; and fragments with at least 6 amino acid length, preferably at least 9 ami acid length starting from the position of: 3, 10, 14, 17, 24, 46, 59, 133, 155, 220, 270, 312, 233, 2, 22, 31, 62, 65, 122, 140, 155, 162, 170, 189, 235, 248, 260, 286, 298, 156, 183 and 325 of Seq ID No 65; 5-26, 29-50, 61, 65-74, 89-96, 140-147, 153-162, 183-188, 191-197, 203-210, 213-225, 1-9, 30-38, 53-63, 70-78, 92-107, 1 149, 158-166, 174-191, 205-224 and 97-113 of Seq ID No 66; and fragments with at least 6 amino a length, preferably at least 9 amino acid length starting from the position of: 31, 33, 39, 56, 63, 78, 1 136, 196, 14, 35, 38, 55, 97, 98, 146, 156, 158, 215, 88 and 214 of Seq ID No 66; 31-36, 46-54, 65-80, 86-1 168-175, 179-186, 188-194, 200-208, 210-216, 225-231, 243-257, 289-296, 362-387, 460-474, 476-486, 504-5 518-525, 569-579, 581-600, 665-684, 688-694, 700-705, 717-735, 182-193, 202-211, 279-294, 311-319, 369-3 468-476, 547-558, 579-587, 681-700, 731-740, 92-177 and 591-604 of Seq ID No 67; and fragments wit least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 28, 285, 309, 321, 376, 379, 388, 468, 475, 479, 500, 571, 624, 668, 716, 360, 455, 669, 185, 190, 204, 264, 281, 2 478, 502, 588, 675, 680, 716 and 730 of Seq ID No 67; 4-9, 17-24, 27-52, 66-77, 91-98, 104-124, 127-139, 1 199, 211-219, 221-228, 234-244, 246-255, 263-286, 303-312, 316-321, 337-346, 356-362, 367-372, 377-390, 4 416, 449-459, 465-479, 491-501, 503-508, 523-541, 551-558, 560-565, 31-69, 115-127, 132-143, 145-165, 176-1 190-204, 212-220, 266-286, 304-316, 403-423, 440-456, 523-544 and 9-22 of Seq ID No 68; and fragme with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position 17, 24, 31, 45, 53, 56, 63, 69, 107, 129, 150, 171, 178, 189, 191, 217, 255, 273, 277, 305, 312, 451, 458, 470, 4 506, 522, 71, 379, 20, 29, 34, 44, 119, 133, 276, 284, 300, 328, 404, 465, 470, 529, 543, 182 and 551 of Seq No 68; 34-42, 52-63, 71-87, 112-120, 142-147, 154-159, 166-177, 180-197, 204-224, 237-256, 260-268, 280- 312-324, 338-343, 372-412, 456-463, 479-490, 494-504, 506-512, 518-524, 538-548, 562-573, 585-591, 597- 674-690, 703-712, 714-740, 749-766, 95-103, 114-123, 180-195, 205-220, 240-248, 370-400, 481-495, 588- 707-715, 750-765, 160-253 and 630-717 of Seq ID No 69; and fragments with at least 6 amino acid len preferably at least 9 amino acid length starting from the position of: 179, 206, 209, 213, 216, 255, 300, 304, 324, 365, 369, 373, 376, 377, 380, 381, 384, 562, 694, 720, 721, 729, 749, 752, 755, 197, 330, 559, 600, 714, 751, 91, 111, 140, 167, 191, 315, 388, 393, 402, 458, 463, 587, 720, 762 and 748 of Seq ID No 69; 4 50-55, 59-67, 73-83, 91-98, 101-109, 131-145, 230-236, 267-273, 293-300, 303-310, 349-354, 375-397, 404- 434-441, 445-452, 456-468, 479-485, 487-512, 544-568, 571-579, 593-599, 604-610, 614-621, 642-656, 665- 706-716, 729-736, 748-756, 780-795, 797-814, 827-844, 850-861, 864-882, 889-900, 906-933, 6-23, 28-36, 6 134-150, 182-192, 227-236, 306-316, 340-350, 376-387, 421-435, 449-460, 527-535, 553-569, 587-595, 641- 668-676, 683-694, 743-755, 800-819, 843-865, 861-886, 894-915, 929-938 and 603-669 of Seq ID No 70; fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from position of: 7, 8, 15, 73, 80, 133, 134, 138, 182, 194, 271, 272, 298, 432, 438, 457, 458, 487, 490, 527, 548, 616, 644, 647, 667, 741, 782, 801, 829, 866, 126, 259, 792, 15, 20, 133, 155, 160, 232, 299, 458, 464, 552, 558, 605, 607, 654, 670, 672, 768, 810, 840, 852, 877, 900, 167, 380, 425, 593 and 907 of Seq ID No 70; 4-32, 7 90-101, 116-132, 144-160, 171-182, 195-200, 227-234, 255-271, 293-300, 313-336, 344-350, 369-375, 381- 413-421, 436-465, 487-496, 503-508, 510-527, 538-546, 552-562, 608-614, 617-636, 663-674, 679-691, 705 734-748, 769-807, 825-834, 848-861, 864-871, 891-902, 7-16, 90-107, 110-137, 170-187, 197-213, 233-251, 287, 291-314, 361-390, 412-425, 451-465, 489-498, 513-521, 570-580, 619-637, 662-679, 713-721, 725-733, 754, 766-781, 790-805, 817-834, 868-883, 888-903 and 529-542 of Seq ID No 71; and fragments with at 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8, 23, 5 128, 169, 178, 239, 263, 290, 297, 310, 324, 331, 339, 365, 398, 436, 443, 450, 470, 485, 488, 513, 514, 520, 669, 711, 723, 771, 824, 849, 895, 316, 861, 118, 135, 196, 225, 284, 290, 370, 454, 489, 492, 521, 557, 624, ~~745, 778, 783, 850, 868, 910, 226 and 383 of Seq ID No 71; 10-18, 30-52, 63-70, 72-79, 96-133, 146-158,~~ 175, 184-193, 203-210, 213-222, 227-234, 237-257, 263-273, 285-291, 297-312, 320-338, 359-378, 385-393,

410, 412-421, 490-510, 521-527, 540-548, 563-571, 573-585, 592-598, 615-620, 632-641, 652-661, 672-679, 704-711, 717-723, 729-736, 742-751, 766-778, 788-808, 817-824, 836-842, 34-56, 73-89, 103-130, 146-154, 184-205, 213-227, 245-257, 258-278, 292-316, 331-341, 358-369, 372-383, 388-397, 410-418, 503-514, 524-530, 548-556, 565-573, 584-595, 637-646, 656-663, 673-686, 734-742, 745-754, 757-768, 770-781, 816-828 and 14-101 of Seq ID No 72; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 27, 32, 36, 65, 109, 112, 120, 127, 186, 249, 250, 262, 267, 297, 301, 353, 360, 367, 410, 418, 436, 465, 472, 505, 518, 522, 565, 576, 585, 638, 645, 650, 676, 687, 724, 745, 756, 763, 795, 164, 411, 510, 560, 569, 647, 766, 780, 14, 39, 48, 65, 74, 129, 175, 215, 217, 229, 230, 240, 253, 257, 262, 269, 308, 317, 322, 327, 352, 371, 372, 373, 374, 417, 443, 454, 472, 514, 525, 567, 629, 637, 657, 662, 683, 698, 731, 744, 752, 763, 769, 787, 790, 802, 815, 819, 26, 102, 381 and 704 of Seq ID No 72; 4-14, 20-33, 36-63, 71-93, 96-104, 106-117, 120-128, 131-147, 161-172, 174-186, 195-210, 212-247, 269-286, 288-301, 306-322, 324-332, 348-354, 356-363, 384-391, 35-66, 70-85, 107-118, 124-132, 165-179, 186-196, 197-205, 276-289, 292-300, 348-368, 369-381, 385-394 and 139-151 of Seq ID No 73; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 34, 41, 50, 53, 109, 127, 134, 153, 165, 271, 286, 297, 340, 384, 80, 321, 334, 354, 33, 57, 110, 153, 178, 276, 284, 383, 79, 99 and 123 of Seq ID No 73; 12-20, 37-48, 51-58, 69-75, 86-98, 113-136, 141-161, 171-216, 222-254, 264-273, 291-301, 311-345, 351-361, 31-39, 40-55, 62-74, 121-137, 148-164, 170-178, 223-253, 309-329, 354-369 and 246-275 of Seq ID No 74; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 46, 95, 103, 110, 143, 156, 178, 186, 190, 236, 242, 244, 291, 294, 315, 333, 353, 125, 183, 256, 326, 3, 68, 82, 102, 131, 177, 185, 190, 193, 223, 224, 244, 250, 295, 340, 349, 354, 88 and 89 of Seq ID No 74; 30-36, 50-56, 96-102, 110-116, 125-131, 162-174, 179-187, 189-201, 223-230, 232-239, 266-278, 320-328, 330-337, 339-350, 388-400, 408-413, 417-423, 435-447, 456-480, 499-524, 526-534, 53-62, 92-107, 192-203, 315-323, 436-452, 464-483, 502-524 and 61-138 of Seq ID No 75; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 126, 174, 225, 267, 309, 316, 320, 337, 436, 466, 467, 473, 474, 14, 128, 143, 228, 347, 494, 2, 52, 112, 201, 209, 217, 230, 235, 236, 337, 381, 395, 413, 419, 454, 466, 510, 515 and 556 of Seq ID No 75; 7-32, 36-56, 77-82, 88-100, 117-144, 153-166, 173-180, 188-226, 256-297, 300-316, 323-337, 339-348, 361-384, 390-427, 438-455, 476-488, 516-523, 535-566, 580-586, 597-607, 615-621, 626-634, 639-649, 654-660, 668-673, 677-688, 707-714, 716-728, 730-742, 746-756, 763-772, 801-808, 820-829, 840-875, 882-888, 895-911, 914-920, 928-948, 953-961, 987-995, 999-1005, 1007-1026, 1053-1060, 1071-1079, 1082-1117, 1123-1129, 6-31, 37-48, 58-69, 90-105, 110-118, 134-142, 146-157, 210-220, 267-276, 291-300, 319-330, 362-372, 393-401, 405-421, 447-456, 463-471, 517-525, 574-582, 597-612, 618-626, 642-650, 656-668, 668-678, 683-695, 725-733, 778-791, 840-849, 894-917, 927-939, 954-963, 966-974, 978-998, 1010-1021, 1056-1067, 1070-1083, 1090-1104 and 325-389 of Seq ID No 76; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 11, 18, 22, 41, 48, 86, 104, 156, 190, 197, 221, 286, 290, 334, 343, 345, 407, 442, 509, 538, 575, 596, 597, 598, 636, 678, 685, 723, 754, 757, 779, 818, 850, 857, 864, 893, 900, 901, 907, 918, 927, 934, 972, 988, 1018, 1025, 1034, 1048, 1065, 1072, 1089, 1094, 1101, 1108, 127, 336, 411, 806, 852, 28, 68, 90, 91, 93, 158, 293, 310, 350, 368, 380, 394, 425, 441, 461, 554, 569, 597, 628, 667, 684, 724, 737, 752, 761, 767, 804, 851, 897, 907, 933, 979, 1030, 1032, 1051, 1075, 1090, 1125, 133, 308, 502, 797, 939 and 960 of Seq ID No 76; 11-19, 34-53, 55-91, 113-119, 122-129, 131-140, 157-170, 173-179, 188-195, 200-206, 208-220, 222-232, 236-244, 250-265, 267-274, 282-290, 293-301, 317-323, 336-343, 355-361, 372-384, 33-54, 69-95, 210-221, 244-254, 257-269 and 324-351 of Seq ID No 77; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 32, 37, 43, 47, 50, 53, 57, 64, 68, 71, 73, 74, 78, 80, 82, 113, 120, 155, 162, 194, 205, 209, 231, 235, 238, 252, 259, 266, 273, 280, 287, 294, 301, 308, 315, 333, 8, 16, 18, 66, 377, 36, 44, 81, 99, 124, 193, 261 and 319 of Seq ID No 77; 31-55, 58-64, 69-75, 81-90, 129-150, 154-167, 179-184, 189-208, 227-237, 248-271, 277-284, 313-340, 350-358, 361-368, 371-378, 384-390, 418-425, 438-444, 455-468, 487-506, 514-523, 525-550, 558-569, 572-578, 588-598, 607-618, 645-651, 653-665, 672-684, 708-715, 717-742, 754-771, 776-782, 786-802, 806-817, 1-9, 31-46, 52-61, 60-78, 132-148, 182-199, 214-229, 249-264, 280-293, 320-341, 347-355, 386-411, 486-502, 553-575, 624-634, 673-689, 690-700, 702-714, 721-735, 736-746, 757-777, 788-798, 810-818 and 90-100 of Seq ID No 78; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 51, 82, 139, 186, 193, 197, 200, 239, 248, 249, 250, 257, 311, 325, 326, 520, 555, 556, 589, 606, 651, 716, 723, 730, 737, 758, 761, 772, 788, 39, 41, 569, 695, 709, 783, 51, 60, 89, 110, 141, 207, 216, 295,

301, 395, 404, 518, 527, 555, 568, 593, 596, 673, 691, 722, 757, 772, 790, 799, 130, 131, 179, 402, 414 and 701 Seq ID No 78;13-19, 22-28, 61-67, 74-81, 86-103, 110-122, 141-155, 162-169, 171-177, 181-186, 192-199, 2(207, 225-238, 246-263, 273-279, 287-300, 307-313, 331-336, 351-367, 370-376, 380-392, 395-402, 415-422, 4 451, 454-465, 473-492, 496-509, 515-523, 541-547, 569-582, 589-601, 613-636, 638-647, 653-679, 702-714, 7 729, 739-748, 768-779, 799-813, 821-828, 832-840, 847-853, 857-873, 886-892, 894-905, 917-926, 958-971, 9 981, 983-989, 997-1004, 1006-1032, 1034-1049, 1054-1061, 1063-1069, 1073-1081, 1083-1095, 1097-1115, 11 1132, 1143-1153, 1164-1171, 1178-1185, 1193-1213, 1216-1251, 1258-1272, 1277-1283, 1305-1317, 1324-13 1333-1355, 1383-1390, 25-43, 81-92, 111-141, 150-159, 213-220, 222-242, 243-254, 256-267, 276-288, 289-3 381-397, 398-409, 422-438, 441-464, 485-500, 515-528, 542-553, 569-585, 591-601, 639-649, 656-664, 709-7 725-734, 739-753, 841-850, 883-893, 902-911, 912-926, 935-948, 960-969, 976-984, 994-1008, 1037-1047, 10 1085, 1100-1108, 1124-1134, 1167-1179, 1194-1203, 1220-1254, 1258-1277, 1308-1319, 1348-1366 and 273-2 of Seq ID No 79; **and fragments with at least 6 amino acid length, preferably at least 9 amino a length starting from the position of:** 107, 110, 112, 133, 152, 200, 204, 223, 244, 251, 271, 289, 291, 305, 3 360, 380, 407, 422, 428, 440, 491, 507, 512, 536, 616, 625, 628, 648, 650, 665, 668, 748, 768, 784, 797, 801, 8 858, 859, 903, 910, 913, 925, 932, 959, 960, 968, 993, 1008, 1020, 1068, 1072, 1138, 1141, 1142, 1193, 1201, 12 1226, 1237, 1261, 1271, 1311, 1348, 1349, 1377, 126, 375, 433, 477, 608, 658, 852, 1106, 1121, 1303, 1362, 102, 151, 164, 169, 211, 229, 245, 274, 279, 285, 333, 348, 361, 382, 391, 397, 428, 447, 453, 480, 496, 590, 5 595, 615, 623, 629, 638, 664, 669, 672, 738, 744, 775, 789, 840, 910, 917, 939, 966, 977, 1057, 1084, 1096, 11 1127, 1128, 1145, 1163, 1167, 1202, 1214, 1238, 1244, 1260, 1279, 1335, 145, 355, 961, 1053, 1103 and 124 Seq ID No 79; 16-23, 25-47, 49-59, 64-72, 79-91, 95-105, 113-122, 133-145, 148-162, 169-176, 179-188, 1 200, 202-218, 232-239, 250-283, 299-333, 337-344, 349-355, 364-406, 430-437, 439-449, 452-460, 464-490, 4 503, 505-530, 533-562, 12-21, 28-39, 52-67, 115-124, 189-204, 224-232, 234-242, 263-284, 302-322, 363-3 389-397, 446-463, 479-488, 513-522, 528-552 and 401-419 of Seq ID No 80; **and fragments with at lea amino acid length, preferably at least 9 amino acid length starting from the position of:** 23, 30, 58, 84, 97, 98, 120, 123, 133, 162, 169, 189, 215, 218, 236, 309, 312, 316, 365, 372, 384, 388, 391, 426, 446, 453, 4 466, 478, 508, 513, 515, 523, 530, 536, 543, 554, 333, 467, 13, 19, 115, 130, 181, 195, 225, 262, 270, 275, 311, 325, 342, 390, 391, 398, 461, 530, 116, 188 and 229 of Seq ID No 80;8-16, 36-54, 59-76, 85-92, 104-124, 1 180, 199-248, 255-298, 300-307, 324-339, 356-373, 381-393, 402-442, 448-455, 18-27, 36-56, 101-120, 145- 165-173, 179-189, 239-255, 255-270, 330-346, 355-375, 383-394, 403-421 and 83-232 of Seq ID No 81; **fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from position of:** 5, 102, 149, 156, 160, 164, 185, 186, 204, 208, 211, 221, 232, 264, 270, 273, 277, 280, 284, 287, 329, 362, 387, 398, 402, 404, 422, 429, 431, 449, 37, 298, 359, 9, 17, 35, 40, 41, 105, 111, 146, 166, 234, 279, 384, 412 and 365 of Seq ID No 81; 29-69, 71-88, 95-104, 106-130, 143-189, 205-232, 24-40, 46-64, 65-79 105, 121-129, 144-199, 206-236 and 182-199 of Seq ID No 82; **and fragments with at least 6 amino length, preferably at least 9 amino acid length starting from the position of:** 30, 37, 66, 77, 81, 84, 118, 141, 144, 145, 146, 149, 150, 153, 167, 169, 170, 178, 196, 213, 215, 220, 13, 21, 39, 44, 62, 75, 78, 97, 124, 145, 148, 154, 177, 190, 207, 22 and 216 of Seq ID No 82; 4-46, 51-66, 77-88, 102-110, 115-126, 142- 171-181, 183-192, 202-212, 227-234, 251-261, 263-278, 283-316, 319-325, 336-352, 362-371, 386-393, 399- 410-425, 427-437, 441-450, 457-464, 471-476, 490-496, 514-521, 549-557, 571-578, 601-611, 618-623, 627- 657-670, 672-689, 696-704, 726-740, 742-756, 765-776, 778-784, 792-801, 822-836, 862-868, 875-881, 887 914-919, 941-948, 963-969, 971-978, 996-1004, 1007-1016, 1036-1051, 1068-1080, 1082-1090, 1092-1098, 1 1127, 1135-1144, 1156-1177, 1181-1195, 1197-1206, 1214-1231, 1243-1263, 1278-1284, 1295-1303, 1305- 1337-1346, 1355-1374, 1376-1383, 1406-1423, 1455-1463, 1465-1489, 1506-1518, 1527-1552, 1555-1570, 1 1589, 1-28, 109-124, 208-220, 261-280, 286-296, 310-324, 398-405, 425-433, 439-454, 504-517, 535-555, 570 599-614, 620-630, 691-699, 711-719, 729-739, 751-760, 783-791, 843-855, 878-886, 890-900, 940-955, 984- 1007-1026, 1065-1073, 1106-1122, 1136-1149, 1188-1198, 1203-1211, 1227-1235, 1249-1256, 1298-1308, 1 1392, 1398-1409, 1414-1429, 1436-1444, 1456-1490, 1504-1521, 1530-1547, 1592-1609 and 911-935 of Se No 83; **and fragments with at least 6 amino acid length, preferably at least 9 amino acid length sta from the position of:** 26, 33, 79, 170, 200, 265, 290, 297, 302, 304, 333, 334, 377, 412, 414, 415, 431, 436 465, 481, 494, 536, 546, 568, 605, 678, 690, 697, 703, 724, 729, 730, 735, 737, 767, 776, 797, 840, 861, 938 999, 1072, 1079, 1085, 1094, 1113, 1160, 1163, 1180, 1188, 1195, 1217, 1245, 1250, 1273, 1302, 1358, 1362, 1401, 1408, 1465, 1469, 1481, 1507, 178, 960, 1034, 6, 21, 38, 159, 204, 248, 260, 306, 337, 349, 384, 425

458, 481, 502, 521, 546, 605, 690, 730, 731, 819, 860, 915, 946, 967, 1007, 1018, 1065, 1113, 1187, 1188, 1205,
1223, 1409, 1414, 1495, 1526, 1531, 1537, 101, 255, 1421, 1457, 1538, 1580 and 1589, of Seq ID No 83;15-25,
41-102, 111-117, 127-134, 145-170, 194-201, 207-225, 10-30, 36-44, 46-59, 57-98, 122-138, 144-160, 162-173,
194-217 and 118-131 of Seq ID No 84; and fragments with at least 6 amino acid length, preferably at
least 9 amino acid length starting from the position of: 12, 16, 37, 46, 61, 82, 121, 128, 149, 157, 162, 197,
204, 212, 39, 2, 23, 53, 68, 97, 107, 121, 127, 156, 169, 196, 9, 13 and 114 of Seq ID No 84; 7-54, 65-94, 97-103,
154-163, 170-180, 182-199, 216-222, 227-234, 243-256, 267-273, 286-298, 314-322, 324-353, 363-380, 393-401,
424-431, 434-441, 447-470, 475-495, 506-532, 540-548, 554-592, 594-607, 609-617, 619-626, 628-634, 656-662,
8-31, 43-59, 61-75, 93-104, 126-144, 179-201, 244-254, 289-302, 330-338, 364-382, 413-421, 428-466, 476-525,
582-599, 602-619 621-632 and 115-128 of Seq ID No 85; and fragments with at least 6 amino acid length,
preferably at least 9 amino acid length starting from the position of: 9, 10, 13, 35, 46, 76, 77, 83, 151, 165,
179, 187, 195, 283, 326, 338, 342, 360, 365, 368, 375, 415, 450, 485, 508, 556, 565, 569, 576, 602, 5, 20, 130, 181,
251, 271, 288, 294, 333, 355, 356, 364, 446, 451, 467, 483, 486, 523, 544, 611, 214, 219, 323, 399, 424 and 458, of
Seq ID No 85; 5-21, 32-56, 88-99, 117-124, 128-138, 143-150, 168-180, 183-189, 196-213, 220-240, 254-263,
266-289, 300-313, 321-330, 335-358, 361-371, 380-398, 50-65, 67-87, 96-104, 144-153, 156-164, 169-177, 199-
220, 259-289, 324-333, 339-360, 372-385 and 74-93 of Seq ID No 86; and fragments with at least 6 amino
acid length, preferably at least 9 amino acid length starting from the position of: 26, 33, 49, 88, 96, 129,
169, 170, 198, 257, 268, 281, 337, 342, 366, 391, 393, 39, 122, 248, 76, 106, 117, 185, 190, 198, 238, 257, 266, 280,
341, 344, 350, 367, 304 and 384 of Seq ID No 86; 12-23, 44-50, 54-60, 91-97, 103-109, 119-125, 131-137, 141-
151, 172-183, 201-226, 230-238, 252-265, 315-321, 331-345, 360-370, 376-386, 392-406, 410-416, 422-431, 133-
159, 208-222, 354-368 and 1-88 of Seq ID No 87; and fragments with at least 6 amino acid length,
preferably at least 9 amino acid length starting from the position of: 47, 134, 140, 143, 203, 204, 210, 254,
355, 358, 359, 362, 369, 417, 119, 17, 128, 129, 141, 143, 153, 208, 232, 245, 278, 301, 313, 327, 328, 384 and 395
of Seq ID No 87; 4-16, 29-36, 39-64, 69-75, 79-87, 90-122, 126-134, 139-173, 184-190, 195-203, 206-213, 216-
228, 234-246, 250-257, 260-266, 274-282, 291-312, 318-325, 340-345, 348-361, 364-388, 399-437, 439-448, 451-
464, 467-473, 480-510, 514-520, 534-553, 561-574, 579-589, 593-599, 616-655, 658-671, 3-12, 23-38, 27-38, 43-
56, 93-107, 123-137, 144-154, 175-199, 229-244, 288-303, 308-316, 323-337, 410-423, 455-473, 488-496, 531-551,
560-577, 577-591, 619-637, 646-660, 664-672 and 553-570 of Seq ID No 88; and fragments with at least 6
amino acid length, preferably at least 9 amino acid length starting from the position of: 36, 101, 123,
129, 136, 146, 156, 160, 194, 205, 219, 236, 245, 283, 289, 350, 402, 413, 437, 475, 505, 517, 542, 585, 605, 620,
627, 657, 34, 52, 88, 358, 540, 656, 3, 8, 13, 32, 82, 105, 111, 117, 137, 167, 173, 180, 182, 262, 300, 306, 350, 409,
412, 423, 499, 500, 563, 568, 581, 585, 627, 628, 554 and 638 of Seq ID No 88; 4-31, 50-80, 83-93, 97-103, 111-
116, 123-132, 134-163, 170-199, 205-210, 215-220, 230-247, 249-278, 280-308, 311-329, 337-347, 349-358, 365-
371, 376-401, 417-430, 434-446, 459-505, 511-518, 527-535, 537-545, 547-565, 573-581, 592-601, 1-17, 20-30,
66-80, 100-119, 139-150, 171-182, 186-198, 207-221, 228-242, 258-274, 286-308, 314-330, 337-352, 355-376,
383-391, 417-432, 437-446, 462-473, 479-488, 496-507, 514-522, 541-554, 557-565, 576-585, 589-605, 49-60 and
582-607 of Seq ID No 89; and fragments with at least 6 amino acid length, preferably at least 9 amino
acid length starting from the position of: 4, 65, 66, 120, 121, 144, 170, 174, 208, 226, 233, 276, 278, 285, 286,
298, 336, 348, 355, 363, 382, 384, 395, 457, 458, 494, 501, 578, 133, 278, 294, 551, 53, 89, 110, 159, 186, 232, 290,
324, 406, 431, 458, 463, 480, 490, 513, 541, 549, 558, 585, 22, 137, 152, 189, 227, 255, 261, 291, 419 and 569 of
Seq ID No 89; 9-60, 67-73, 79-93, 109-122, 134-142, 144-153, 165-192, 197-225, 235-244, 259-279, 289-299,
308-317, 321-332, 338-347, 350-361, 373-387, 402-409, 411-421, 439-445, 450-456, 462-468, 470-479, 490-501,
503-516, 16-27, 49-60, 99-122, 136-145, 148-162, 186-194, 213-221, 225-246, 261-275, 281-292, 353-361, 390-
401, 451-470, 486-494, 497-516 and 478-490 of Seq ID No 90; and fragments with at least 6 amino acid
length, preferably at least 9 amino acid length starting from the position of: 15, 22, 28, 29, 48, 49, 106,
107, 114, 147, 170, 177, 188, 208, 209, 212, 256, 280, 287, 316, 451, 468, 489, 33, 217, A03: 36, 98, 124, 136, 142,
153, 177, 188, 251, 262, 291, 320, 323, 383, 417, 464, 487, 491, 492, 505, 44, 86, 146, 411, 437 and 499 of Seq ID
No 90; 4-10, 16-28, 3-14, 16-30 and 2-16 of Seq ID No 91; and fragments with at least 6 amino acid
length, preferably at least 9 amino acid length starting from the position of: 1 and15 of Seq ID No 91; 8-
18, 20-30 and 7-15 of Seq ID No 92; 4-16, 18-27, 2-13, 20-30 and 10-29 of Seq ID No 93; and fragments
with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of:
22 and 1 of Seq ID No 93; 36-57, 62-92, 46-66 and 27-35 of Seq ID No 94; and fragments with at least 6

amino acid length, preferably at least 9 amino acid length starting from the position of: 84 of Seq No 94; 4-18, 1-16 and 5-12 of Seq ID No 95; and fragments with at least 6 amino acid length, preferab at least 9 amino acid length starting from the position of: 1, 9 and 2 of Seq ID No 95; 13-27, 38-52, 1- 11-25, 27-37 and 17-36 of Seq ID No 96; and fragments with at least 6 amino acid length, preferably least 9 amino acid length starting from the position of: 16, 37 and 20 of Seq ID No 96; 4-17, 27-40, 55- 9-25, 34-46, 50-64 and 47-62 of Seq ID No 97; and fragments with at least 6 amino acid leng preferably at least 9 amino acid length starting from the position of: 7, 10, 11, 14 and 58 of Seq ID 97; 4-9, 1-10 of Seq ID No 98; 3-14 and 7-20 of Seq ID No 99; and fragments with at least 6 amino a length, preferably at least 9 amino acid length starting from the position of: 2 and 1 of Seq ID No 99; 12, 24-29, 22-30 and 7-21 of Seq ID No 100; and fragments with at least 6 amino acid length, prefera at least 9 amino acid length starting from the position of: 4 and 9 of Seq ID No 100; 14-30, 15-30 and 18 of Seq ID No 101; and fragments with at least 6 amino acid length, preferably at least 9 amino a length starting from the position of: 1 and 20 of Seq ID No 101; 3-17 of Seq ID No 102; and fragme with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position 1 of Seq ID No 102; 4-27, 31-59, 75-86, 93-103, 105-110, 15-44, 51-61, 79-95 and 41-50 of Seq ID No 1 and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fr the position of: 11, 15, 24, 28, 31, 35, 36, 42, 48, 49, 53, 78, 79, 97, 20, 28, 35, 37, 43, 49, 60, 65, 77, 85, 86, and 103 of Seq ID No 103; 4-13 and 2-14 of Seq ID No 104; and fragments with at least 6 amino a length, preferably at least 9 amino acid length starting from the position of: 7 and 10 of Seq ID No 1 4-15, 17-23, 39-52, 4-13, 16-29, 40-50 and 33-41 of Seq ID No 105; and fragments with at least 6 ami acid length, preferably at least 9 amino acid length starting from the position of: 3, 38, 14 and 41 of S ID No 105; 4-25 of Seq ID No 106; 8-19, 40-47, 67-86, 88-125, 15-25, 48-59, 64-80, 108-118 and 60-70 of S ID No 107; and fragments with at least 6 amino acid length, preferably at least 9 amino acid len starting from the position of: 7, 110, 16, 34 and 109 of Seq ID No 107; 4-27, 41-46, and 30-47 of Seq ID 108; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length start from the position of: 19, 1 and 23 of Seq ID No 108; 21-28, 34-43, 8-16 and 23-42 of Seq ID No 109; fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from position of: 34, 19, 28 and 39 of Seq ID No 109; 8-20, 24-37, 39-50, 61-67, 69-91, 4-16, 31-42, 84-93 and 59 of Seq ID No 110; and fragments with at least 6 amino acid length, preferably at least 9 amino a length starting from the position of: 4, 24, 79, 83, 7, 25, 71, 79 and 91 of Seq ID No 110; 4-25, 31-39, 59- 100-118, 120-129, 26-40, 49-57, 66-95, 97-128, 131-139, 38-47 of Seq ID No 111; and fragments with at l 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8, 24, 61, 72, 103, 112, 3, 39, 74, 110 and 119 of Seq ID No 111; 7-24, 32-43, 45-57, 32-48 and 27-43 of Seq ID No 1 and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fr the position of: 14, 18, 38, 47 and 14 of Seq ID No 112; 4-18, 20-26, 31-37, 3-17, 33-43 and 34-53 of Seq No 113; and fragments with at least 6 amino acid length, preferably at least 9 amino acid len starting from the position of: 3, 7, 10 and 9 of Seq ID No 113; 15-23, 25-39, 43-50, 62-70, 16-32, 61-73 67-84 of Seq ID No 114; and fragments with at least 6 amino acid length, preferably at least 9 am acid length starting from the position of: 8 and 64 of Seq ID No 114; 4-13, 28-42, 3-14, 28-39 and 1-2 Seq ID No115; and fragments with at least 6 amino acid length, preferably at least 9 amino acid len starting from the position of: 31, 7 and 5 of Seq ID No115; 4-10, 19-26, 21-29 and 5-13 of Seq ID No 4-22, 40-46, 51-57, 64-76, 2-10, 45-53, 58-72, 73-82 and 33-45 of Seq ID No117; and fragments with at l 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 35, 76, and 66 of Seq ID No117; 12-24, 27-42, 13-30, 34-44 and 1-9 of Seq ID No 118; and fragments with at l 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 36, 15 an of Seq ID No 118; 4-55, 5-15, 17-33 and 26-45 of Seq ID No 119; and fragments with at least 6 amino length, preferably at least 9 amino acid length starting from the position of: 14 and 53 of Seq ID 119; 31-42, 45-52, 86-92, 8-16, 35-52, 83-91 and 27-93 of Seq ID No 120; and fragments with at lea amino acid length, preferably at least 9 amino acid length starting from the position of: 86, 56, 21 a of Seq ID No 120; 237 – 256, 508 – 530 of Seq ID No 61; 227 – 239 of Seq ID No 62; 141 – 160, 168 – ~~155 – 173 of Seq ID No 63; 101 – 124, 161 – 187, 59 – 85, 80 – 106 of Seq ID No 64; 97 – 112 of Seq ID~~ 66; 139 – 165 of Seq ID No 67; 10 – 21 of Seq ID No 68; 667 – 688, 677 – 696, 161 – 187, 183 – 209, 205 –

226 – 252 of Seq ID No 69; 603 – 629, 622 – 648, 643 – 669 of Seq ID No 70; 529 – 541 of Seq ID No 71; 12 – 34, 29 – 51, 46 – 67, 62 – 83 of Seq ID No 72; 139 – 151 of Seq ID No 73; 246 – 262, 251 – 275 of Seq ID No 74; 61 – 84, 79 – 102, 97 – 120, 115 – 138 of Seq ID No 75; 325 – 350, 345 – 370, 365 – 389 of Seq ID No 76; 324 – 349, 336 – 351 of Seq ID No 77; 90 – 100 of Seq ID No 78; 274 – 290 of Seq ID No 79; 401 – 419 of Seq ID No 80; 84 – 107, 101 – 123, 117 – 139 of Seq ID No 81; 182 – 199 of Seq ID No 82; 911 – 935 of Seq ID No 83; 118 – 131 of Seq ID No 84; 115 – 128 of Seq ID No 85; 74 – 93 of Seq ID No 86; 21 – 43, 54 – 76 of Seq ID No 87; 554 – 570 of Seq ID No 88; 478 – 490 of Seq ID No 90; 2 – 14 of Seq ID No 91; 7 – 15 of Seq ID No 92; 10 – 28 of Seq ID No 93; 27 – 34 of Seq ID No 94; 17 – 35 of Seq ID No 96; 47 – 61 of Seq ID No 97; 1-10 of Seq ID No 98; 7-20 of Seq ID No 99; 7-20 of Seq ID No 100; 3-17 of Seq ID No 101; 3-17 of Seq ID No 102; 41-50 of Seq ID No 103; 2-14 of Seq ID No 104; 33-41 of Seq ID No 105; 4-25 of Seq ID No 106; 60-69 of Seq ID No 107; 23-41 of Seq ID No 109; 42-59 of Seq ID No 110; 38-46 of Seq ID No 111; 27-43 of Seq ID No 112; 34-53 of Seq ID No 113; 67-84 of Seq ID No 114; 1-20 of Seq ID No 115; 33-45 of Seq ID No 117; 26-45 of Seq ID No 119; 27-53 of Seq ID No 120, and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences.

The present invention also provides a process for producing a *C. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *C. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLLLLLKLK, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *C. pneumoniae* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention, is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to th present invention.

Moreover, the present invention provids a method for producing an antibody according to the preser invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmun serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to furth purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to th present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmu serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens o fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally furth purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation a medicament for treating or preventing *C. pneumoniae* infections.

According to another aspect the present invention provides an antagonist, which binds to hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment ther according to the present invention may be identified by a method comprising the following steps:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragm thereof according to the present invention with a candidate antagonist under conditions permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen fragment, in the presence of a component capable of providing a detectable signal in respons the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragm thereof; and
b) detecting the presence or absence of a signal generated in response to the binding of antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reac antigen or a fragment thereof according to the present invention to its interaction partner may identified by a method comprising the following steps:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof accor to the present invention,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragn thereof, especially an antibody according to the present invention,

c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
d) providing a candidate antagonist,
e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *C. pneumoniae* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *C. pneumoniae* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *C. pneumoniae*. Thus, the present invention fulfils a widely felt demand for *C. pneumoniae* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *C. pneumoniae* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *C. pneumoniae* or a sustained T-cell response capable of eradicating infected cells of the host. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *C. pneumoniae*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction Chlamydial proteins or peptides with the antibodies present in human sera. The antibodies produc against *C. pneumoniae* by the human immune system and present in human sera are indicative of the *vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins identified by the bacterial surface display expression libraries using pools of pre-selected sera, a processed in a second and third round of screening by individual selected or generated sera. Thus t present invention supplies an efficient, relevant, comprehensive set of chlamydial antigens as pharmaceutical composition, especially a vaccine preventing infection by *C. pneumoniae*.

In the antigen identification program for identifying a comprehensive set of antigens according to present invention, at least two different bacterial surface expression libraries are screened with seve serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). T antibody pools are derived from a serum collection, which has been tested against antigenic compour of *C. pneumoniae* - highly enriched outer membrane preparation for ELISA and elementary body (isolated from *C. pneumoniae* infected eukaryotic cells. Preferably, two distinct serum collections are us 1. For antigen identification: sera from patients with clinical symptomes characterized with high anti *pneumoniae* antibody levels and 2. For antigen validation: sera from healthy people and patie characterized with low, medium and high anti-*C. pneumoniae* antibody levels. Sera have to react w multiple Chlamydia-specific antigens in order to be considered hyperimmune and therefore relevan the screening method applied for the present invention. Sera with low specific antibodies serve negative controls.

The expression libraries as used in the present invention should allow expression of all potential antig e.g. derived from all secreted and surface proteins of *C. pneumoniae*. Bacterial surface display libraries be represented by a recombinant library of a bacterial host displaying a (total) set of expressed pep sequences of *C. pneumoniae* on two selected outer membrane proteins (LamB and FhuA) at the bacte host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombir expression libraries is that the identified hyperimmune serum-reactive antigens may be insta produced by expression of the coding sequences of the screened and selected clones expressing hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning s necessary.

The comprehensive set of antigens identified by the described program according to the pre invention is analysed further by one or more additional rounds of screening. Therefore indivi antibody preparations or antibodies generated against selected peptides, which were identifie immunogenic are used. According to a preferred embodiment the individual antibody preparations the second round of screening are derived from patients who have suffered from infection wit *pneumoniae*, especially from patients who show an IgG antibody titer above a certain minimum level example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, espec higher than 95 percentile of the human (patient or healthy individual) sera tested. These thresholds above of a titer of 400, meaning that individual serum samples can be diluted more than 400 times to positive serological (ELISA) results. Using such high titer individual antibody preparations in the sec screening round allows a very selective identification of the hyperimmune serum-reactive antigens fragments thereof from *C. pneumoniae*.

Following the comprehensive screening procedure, the selected antigenic proteins, produced as synt peptides corresponding to identified immunogenic epitopes are tested in a second screening by a seri ELISA assays for the assessment of their immunogenicity with a large human serum collection.

It is important that the individual antibody preparations (which may also be the selected serum) all ~~selective identification of the most promising candidates of all the hyperimmune serum-reactive ant~~ from all the promising candidates from the first round. Therefore, preferably at least 10 indiv

antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. Of course, it is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. On the other hand, if a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) is recognized by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations, identification of the hyperimmune serum-reactive antigen is also selective enough for a proper identification. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *C. pneumoniae* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgG titer above 200, especially above 400 measured by a commercially available IgG ELISA kit.

The antibodies produced against Chlamydia by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes recognized by serum antibodies can be based on sequences as short as 4-5 amino acids. Of course it does not necessarily mean that these short peptides are capable of inducing the given antibody *in vivo*. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce T cells and antibodies against the selected proteins *in vivo*.

C. pneumoniae as an obligate intracellular parasite, has a unique biphasic life cycle with a smaller extracellular form, the infectious, non-replicating, relatively metabolically inert elementary body (EB), and a larger intracellular form, the infectious, replicating and metabolically active reticulate body. The EBs attach to susceptible host cells and are taken up by phagocytosis. Within the cell they revert to reticulate bodies and replicate before they revert to EBs prior to host cell lysis. Although the immune correlates of protection against *C. pneumoniae* are not well defined, studies using mouse models faithfully mimicking important aspects of human infection indicate that particularly CD8+ T cells and IFN-γ are critical for protection {Wizel, B. et al., 2002}. Since *C. pneumoniae* resides in the membrane bound vacuole, the preferred antigens have to reach the cytosol of infected cells and need to be subsequently recognized as MHC class I-peptide complex by CD8+ T cells. Most of the previously reported antigens – which seem to be therefore capable of reaching the cytosol - are located on the cell surface (e.g. outer membrane proteins) or are secreted (e.g. {Murdin, A. et al., 2000}; {Wizel, B. et al., 2002}). It has been shown that *C. pneumoniae* peptide specific CD8+ CTL and their soluble factors can inhibit chlamydial growth in vitro {Wizel, B. et al., 2002}. In addition, to the T cell-mediated immune response, antibodies against cell wall proteins induced by B cell epitopes may aid the T cell-mediated immune response and serve multiple purposes: they may inhibit adhesion, interfere with nutrient acquisition, inhibit immune evasion and promote phagocytosis {Hornef, M. et al., 2002}. Antibodies against secreted proteins are potentially beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within chlamydial species. The described experimental approach is based on the use of antibodies specifically induced by *C. pneumoniae* purified

from human serum. The antigens identified by the genomic screens are thereby shown to be expressed ir vivo in the host and to be capable of inducing an antibody response. Since it has been shown for many proteins that B cell and T cell epitopes reside in the same protein, the most promising candidate identified by the genomic screens can be further evaluated for the induction of a potent T cell response ir vivo. As a first step, bioinformatic analyses have been used to identify potential T cell epitopes in silico which can then be tested in the appropriate murine model of infection. Thus the present inventio combines the experimental identification of immunogenic proteins with the bioinformatic prediction of T cell epitopes in order to provide candidates for an efficient vaccine to treat or prevent Chlamydia infections.

The method according to the present invention provides thus an optimal tool for the identification c chlamydial antigenic proteins as vaccine candidates. The selection of antigens as provided by the prese invention is also well suited to identify those proteins that harbour B and T cell epitopes necessary t induce a protective immune resonse against infection by *C. pneumoniae* in animal models or in humans.

According to the antigen identification method used herein, the present invention can surprising provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens an fragments thereof of *C. pneumoniae*, among other things, as described below. According to one aspect, th invention particularly relates to the nucleotide sequences encoding hyperimmune serum reacti antigens which sequences are set forth in the Sequence listing Seq ID No: 1-60 and the correspondi encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in th Sequence Listing Seq ID No 61-120.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhib 70% identity over their entire length to a nucleotide sequence set forth with Seq ID No 31-60. Most high preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over th entire length to a nucleic acid molecule set forth with Seq ID No 31-60. In this regard, nucleic ac molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same a particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98 and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferr with 100% identity being especially preferred. Moreover, preferred embodiments in this respect a nucleic acids, which encode hyperimmune serum reactive antigens or fragments thereof (polypeptid which retain substantially the same biological function or activity as the mature polypeptide encoded said nucleic acids set forth in the Seq ID No 31-60.

Identity, as known in the art and used herein, is the relationship between two or more polypept sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In art, identity also means the degree of sequence relatedness between polypeptide or polynucleot sequences, as the case may be, as determined by the match between strings of such sequences. Iden can be readily calculated. While there exist a number of methods to measure identity between t polynucleotide or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Seque Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determ identity are designed to give the largest match between the sequences tested. Methods to determ identity are codified in computer programs. Preferred computer program methods to determine iden between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 19 BLASTP, BLASTN, and FASTA {Altschul, S. et al., 1990}.

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at l 96% identity to the nucleic acid sequence set forth with Seq ID No 5, 7-8, 14-16, 18-22, 24-27, 29-30.

The nucleic acid molecule according to the present invention can, as a second alternative, also be a nucleic acid molecule, which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley & Sons, 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C
- Moderate stringency wash in 0.2xSSC, O.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_M of 96°C. For 1% mismatch, the T_M is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein are in principle applicable as well.

Of course, all nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Chlamydia pneumoniae* strain AR39 genome ({Read, T. et al., 2000}; GenBank accession AE002161) and/or any other published *C. pneumoniae* genome sequence or parts thereof, especially of the strains CWL029 ({Kalman, S. et al., 1999}; GenBank accession AE001363) and J138 ({Shirai, M. et al., 2000}; GenBank accession AB036071-AB036089). Specifically preferred non-identical nucleic acid residues are residues, which lead

to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode for polypeptide having at least 1, preferably at least 2, preferably at least 3 different amino acid residues compared to th published *C. pneumoniae* counterparts mentioned above. Also such isolated polypeptides, bein fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having a least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucle acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of th present invention according to the above outlined first, second, and third alternative. Stringe hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of t nucleic acid molecules according to any nucleic acid molecule of the present invention according to t first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers the fact that preferably the nucleic acids according to the present invention code for the hyperimmu serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic ac molecule is particularly useful in the detection of a nucleic acid molecule according to the prese invention and thus the diagnosis of the respective microorganisms such as *C. pneumoniae* and any disea or diseased condition where this kind of microorganims is involved. Preferably, the hybridisation wou occur or be preformed under stringent conditions as described in connection with the fourth alternati described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DN Thus, for instance, nucleic acid molecule as used herein refers to, among other, single-and doub stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be sing stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and doub stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regi comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the sa molecule or from different molecules. The regions may include all of one or more of the molecules, more typically involve only a region of some of the molecules. One of the molecules of a triple-hel region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbo modified for stability or for other reasons are "nucleic acid molecule" as that term is intended her Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It wil appreciated that a great variety of modifications have been made to DNA and RNA that serve m useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed he embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules o referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are o used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragm both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing o *C. pneumoniae* coding regions, which can be generated by standard cloning methods. To be uniq fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, readily determined by comparing any selected *C. pneumoniae* fragment to the nucleotide sequenc computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *C. pneumoniae* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein and above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deducted *C. pneumoniae* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *C. pneumoniae* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *C. pneumoniae* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *C. pneumoniae,* but trigger the same or preferably an improved T cell response. These epitope are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999},

combined with a systematic exchange of residues potentially interacting with the TCR and testing th resulting sequences with T cells directed against the original epitope. Such a design is possible for skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the origin epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches hav been described in detail for instance by {Hemmer, B. et al., 1999} and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclit epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" ca be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substanc increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immu stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instan nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptid of the present invention and to isolate cDNA and genomic clones of other genes that have a hi sequence similarity to the nucleic acid molecules of the present invention. Such probes generally w comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, a may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. labeled oligonucleotide having a sequence complementary to that of a gene of the present inventior then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents a materials for development of treatments of and diagnostics for disease, particularly human disease, further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the proces herein as described, but preferably for PCR, to determine whether or not the *C. pneumoniae* ge identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. recognized that such sequences will also have utility in diagnosis of the stage of infection and typ infection the pathogen has attained. For this and other purposes the arrays comprising at least one of nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nuc acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundanc *C. pneumoniae.*

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected wit

pneumoniae may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *C. pneumoniae* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *C. pneumoniae*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, RNase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *C. pneumoniae* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification approach. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 91-120 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens, which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 65, 67-68, 74-76, 78-82, 84-87, 89-90 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactiv antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to a antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide whic retains essentially the same or a similar biological function or activity as such hyperimmune seru reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof ma be 1) one in which one or more of the amino acid residues are substituted with a conserved or no conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amir acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of tl amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune seru reactive antigen or fragment thereof is fused with another compound, such as a compound to increase tl half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethyle glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune seru reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof o proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope those skilled in the art from the teachings herein.

The present invention also relates to antigens of different *C. pneumoniae* isolates. Such homologues m easily be isolated based on the nucleic acid and amino acid sequences disclosed herein. The genomes different *C. pneumoniae* isolates are highly conserved as typified by the high degree of identity betwe the two published genomes of *C. pneumoniae* CWL029 and J138 {Shirai, M. et al., 2000}, which w isolated from a patient with pneumonia in the United States before 1987 and from the pharyngeal muc of a 5-year-old boy with acute bronchitis in 1994 in Japan, respectively. There are only 8 regions showi variation between these two strains isolated in different geographic regions and with a large gap in ti The remainder of the sequence is to more than 99.9% identical, indicating the high degree conservation. The third *C. pneumoniae* strain that was sequenced, AR39, which is isolated from a hum case of respiratory tract infection that is epidemiologically distinct from CWL029, confirmed the hi degree of conservation between the *C. pneumoniae* strains {Read, T. et al., 2000}. It is therefore assum that the majority of antigens will be conserved among all *C. pneumoniae* strains. Nevertheless, presence of any antigen can be determined for every strain by appropiate means such as PCR or South blot analysis. In addition, it is possible to determine the variability of a particular antigen in the vari strains by sequencing, as described for example for the *S. pyogenes sic* gene {Hoe, N. et al., 2001}. It is important aspect that the most valuable protective antigens are expected to be conserved among mos not all, various clinical strains.

Among the particularly preferred embodiments of the invention in this regard are the hyperimm serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragme thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypepti comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragme thereof, and variants, analogs and derivatives of the fragments are also encompassed by the pres invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, readily be made using standard techniques, including standard recombinant techniques for produ and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substituti Such substitutions are those that substitute a given amino acid in a polypeptide by another amino aci like characteristics. Typically seen as conservative substitutions are the replacements, one for anot among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and ~~exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and~~ exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and T

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *C. pneumoniae* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of a hyperimmune serum-reactive antigen are selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", "Predicted class II restricted T-Cell epitopes / regions" "Predicted class I restricted T-Cell epitopes / regions",, and "Location of identified immunogenic region" of Table 1; the serum reactive peptide epitopes of Table 2, especially peptides comprising amino acid 18-29, 60-78, 89-95, 100-105, 124-143, 166-180, 187-194, 196-208, 224-242, 285-294, 305-311, 313-320, 351-360, 368-373, 390-403, 411-429, 432-470, 483-489, 513-523, 535-543, 548-564, 579-587, 589-598, 604-612, 622-627, 632-648, 55-84, 190-207, 323-331, 370-390,

551-570, 606-614, 633-647, 39-129, 224-296 and 464-609 of Seq ID No 61; and fragments with at least amino acid length, preferably at least 9 amino acid length starting from the position of: 60, 63, 67, 126, 129, 133, 136, 169, 186, 200, 308, 371, 414, 421, 434, 444, 459, 503, 512, 532, 540, 547, 601, 625, 632, 637, 99, 529, 25, 38, 59, 155, 278, 285, 412, 420, 441, 451, 457, 481, 506, 510, 524, 536, 539, 554, 578, 596, 179 and 604 of Seq ID No 61; 4-29, 31-38, 46-64, 66-80, 109-115, 131-139, 152-160, 170-183, 198-234, 239-2 267-290, 301-313, 318-324, 336-345, 350-365, 380-386, 65-82, 123-165, 268-290, 299-307, 320-329, 336-347, 103, 226-239 and 267-333 of Seq ID No 62; and fragments with at least 6 amino acid length, preferal at least 9 amino acid length starting from the position of: 4, 13, 69, 93, 149, 174, 273, 277, 298, 305, 3 319, 375, 28, 303, 3, 58, 73, 100, 153, 191, 223, 227, 232, 251, 269, 286, 343, 374 and 238 of Seq ID No 62; 33, 35-43, 47-60, 77-92, 113-124, 137-145, 185-196, 66-75 and 92-214 of Seq ID No 63; and fragments w at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 32, 49, 113, 77, 118, 139, 185, 2, 24 and 120 of Seq ID No 63; 47-64, 137-155, 157-167, 182-198, 212-233, 247-2 291-303, 315-337, 345-350, 355-368, 373-379, 58-72, 183-196, 249-261, 315-323, 334-342, 347-356, 358-366 6-188 of Seq ID No 64; and fragments with at least 6 amino acid length, preferably at least 9 amino a length starting from the position of: 135, 160, 183, 184, 204, 249, 256, 293, 296, 318, 319, 356, 372, 94, 60, 159, 163, 189, 204, 220, 233, 300, 333, 335, 356, 362, 198 and 289 of Seq ID No 64; 4-36, 43-49, 60-75, 107, 113-123, 132-172, 186-193, 217-229, 231-250, 260-282, 284-290, 298-312, 315-330, 5-38, 67-77, 113- 134-145, 147-156, 220-236, 271-283, 285-293, 296-304, 309-321 and 159-217 of Seq ID No 65; and fragme with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position 3, 10, 14, 17, 24, 46, 59, 133, 155, 220, 270, 312, 233, 2, 22, 31, 36, 62, 65, 122, 140, 155, 162, 170, 189, 235, 260, 286, 298, 156, 183 and 325 of Seq ID No 65; 5-26, 29-50, 52-61, 65-74, 89-96, 140-147, 153-162, 183- 191-197, 203-210, 213-225, 1-9, 30-38, 53-63, 70-78, 92-107, 141-149, 158-166, 174-191, 205-224 and 97-11 Seq ID No 66; and fragments with at least 6 amino acid length, preferably at least 9 amino acid len starting from the position of: 31, 33, 39, 56, 63, 78, 119, 136, 196, 14, 35, 38, 55, 97, 98, 146, 156, 158, 215 and 214 of Seq ID No 66; 31-36, 46-54, 65-80, 86-102, 168-175, 179-186, 188-194, 200-208, 210-216, 225- 243-257, 289-296, 362-387, 460-474, 476-486, 504-511, 518-525, 569-579, 581-600, 665-684, 688-694, 700- 717-735, 182-193, 202-211, 279-294, 311-319, 369-377, 468-476, 547-558, 579-587, 681-700, 731-740, 92- and 591-604 of Seq ID No 67; and fragments with at least 6 amino acid length, preferably at lea amino acid length starting from the position of: 28, 78, 285, 309, 321, 376, 379, 388, 468, 475, 479, 500, 624, 668, 716, 360, 455, 669, 185, 190, 204, 264, 281, 292, 478, 502, 588, 675, 680, 716 and 730 of Seq ID 67; 4-9, 17-24, 27-52, 66-77, 91-98, 104-124, 127-139, 178-199, 211-219, 221-228, 234-244, 246-255, 263- 303-312, 316-321, 337-346, 356-362, 367-372, 377-390, 402-416, 449-459, 465-479, 491-501, 503-508, 523- 551-558, 560-565, 31-69, 115-127, 132-143, 145-165, 176-187, 190-204, 212-220, 266-286, 304-316, 403- 440-456, 523-544 and 9-22 of Seq ID No 68; and fragments with at least 6 amino acid length, prefer at least 9 amino acid length starting from the position of: 17, 24, 31, 45, 53, 56, 63, 69, 107, 129, 150, 178, 189, 191, 217, 255, 273, 277, 305, 312, 451, 458, 470, 478, 506, 522, 71, 379, 20, 29, 34, 44, 119, 133, 284, 300, 328, 404, 465, 470, 529, 543, 182 and 551 of Seq ID No 68; 34-42, 52-63, 71-87, 112-120, 142- 154-159, 166-177, 180-197, 204-224, 237-256, 260-268, 280-286, 312-324, 338-343, 372-412, 456-463, 479- 494-504, 506-512, 518-524, 538-548, 562-573, 585-591, 597-606, 674-690, 703-712, 714-740, 749-766, 95- 114-123, 180-195, 205-220, 240-248, 370-400, 481-495, 588-596, 707-715, 750-765, 160-253 and 630-717 of ID No 69; and fragments with at least 6 amino acid length, preferably at least 9 amino acid le starting from the position of: 179, 206, 209, 213, 216, 255, 286, 300, 304, 324, 365, 369, 373, 376, 377, 381, 384, 562, 694, 720, 721, 729, 749, 752, 755, 197, 330, 559, 592, 600, 714, 751, 91, 111, 140, 167, 191, 388, 393, 402, 458, 463, 587, 720, 762 and 748 of Seq ID No 69; 4-44, 50-55, 59-67, 73-83, 91-98, 101-109, 145, 230-236, 267-273, 293-300, 303-310, 349-354, 375-397, 404-416, 434-441, 445-452, 456-468, 479-485, 512, 544-568, 571-579, 593-599, 604-610, 614-621, 642-656, 665-678, 706-716, 729-736, 748-756, 780-795, 814, 827-844, 850-861, 864-882, 889-900, 906-933, 6-23, 28-36, 64-75, 134-150, 182-192, 227-236, 306-316, 350, 376-387, 421-435, 449-460, 527-535, 553-569, 587-595, 641-657, 668-676, 683-694, 743-755, 800-819, 865, 861-886, 894-915, 929-938 and 603-669 of Seq ID No 70; and fragments with at least 6 amino length, preferably at least 9 amino acid length starting from the position of: 7, 8, 15, 73, 80, 133, 134, ~~182, 194, 271, 272, 298, 432, 438, 457, 458, 487, 490, 527, 548, 568, 616, 644, 647, 667, 741, 782, 801, 829~~ 126, 259, 792, 15, 20, 133, 155, 160, 232, 299, 458, 464, 552, 558, 560, 605, 607, 654, 670, 672, 768, 810, 840

877, 900, 167, 380, 425, 593 and 907 of Seq ID No 70; 4-32, 73-82, 90-101, 116-132, 144-160, 171-182, 195-200, 227-234, 255-271, 293-300, 313-336, 344-350, 369-375, 381-398, 413-421, 436-465, 487-496, 503-508, 510-527, 538-546, 552-562, 608-614, 617-636, 663-674, 679-691, 705-730, 734-748, 769-807, 825-834, 848-861, 864-871, 891-902, 7-16, 90-107, 110-137, 170-187, 197-213, 233-251, 277-287, 291-314, 361-390, 412-425, 451-465, 489-498, 513-521, 570-580, 619-637, 662-679, 713-721, 725-733, 745-754, 766-781, 790-805, 817-834, 868-883, 888-903 and 529-542 of Seq ID No 71; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8, 23, 53, 57, 128, 169, 178, 239, 263, 290, 297, 310, 324, 331, 339, 365, 398, 436, 443, 450, 470, 485, 488, 513, 514, 520, 614, 669, 711, 723, 771, 824, 849, 895, 316, 861, 118, 135, 196, 225, 284, 290, 370, 454, 489, 492, 521, 557, 624, 632, 745, 778, 783, 850, 868, 910, 226 and 383 of Seq ID No 71; 10-18, 30-52, 63-70, 72-79, 96-133, 146-158, 168-175, 184-193, 203-210, 213-222, 227-234, 237-257, 263-273, 285-291, 297-312, 320-338, 359-378, 385-393, 395-410, 412-421, 490-510, 521-527, 540-548, 563-571, 573-585, 592-598, 615-620, 632-641, 652-661, 672-679, 704-711, 717-723, 729-736, 742-751, 766-778, 788-808, 817-824, 836-842, 34-56, 73-89, 103-130, 146-154, 184-205, 213-227, 245-257, 258-278, 292-316, 331-341, 358-369, 372-383, 388-397, 410-418, 503-514, 524-530, 548-556, 565-573, 584-595, 637-646, 656-663, 673-686, 734-742, 745-754, 757-768, 770-781, 816-828 and 14-101 of Seq ID No 72; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 27, 32, 36, 65, 109, 112, 120, 127, 186, 249, 250, 262, 267, 297, 301, 353, 360, 367, 410, 418, 436, 465, 472, 505, 518, 522, 565, 576, 585, 638, 645, 650, 676, 687, 724, 745, 756, 763, 795, 164, 411, 510, 560, 569, 647, 766, 780, 14, 39, 48, 65, 74, 129, 175, 215, 217, 229, 230, 240, 253, 257, 262, 269, 308, 317, 322, 327, 352, 371, 372, 373, 374, 417, 443, 454, 472, 514, 525, 567, 629, 637, 657, 662, 683, 698, 731, 744, 752, 763, 769, 787, 790, 802, 815, 819, 26, 102, 381 and 704 of Seq ID No 72; 4-14, 20-33, 36-63, 71-93, 96-104, 106-117, 120-128, 131-147, 161-172, 174-186, 195-210, 212-247, 269-286, 288-301, 306-322, 324-332, 348-354, 356-363, 384-391, 35-66, 70-85, 107-118, 124-132, 165-179, 186-196, 197-205, 276-289, 292-300, 348-368, 369-381, 385-394 and 139-151 of Seq ID No 73; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 34, 41, 50, 53, 109, 127, 134, 153, 165, 271, 286, 297, 340, 384, 80, 321, 334, 354, 33, 57, 110, 153, 178, 276, 284, 383, 79, 99 and 123 of Seq ID No 73; 12-20, 37-48, 51-58, 69-75, 86-98, 113-136, 141-161, 171-216, 222-254, 264-273, 291-301, 311-345, 351-361, 31-39, 40-55, 62-74, 121-137, 148-164, 170-178, 223-253, 309-329, 354-369 and 246-275 of Seq ID No 74; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 46, 95, 103, 110, 143, 156, 178, 186, 190, 236, 242, 244, 291, 294, 315, 333, 353, 125, 183, 256, 326, 3, 68, 82, 102, 131, 177, 185, 190, 193, 223, 224, 244, 250, 295, 340, 349, 354, 88 and 89 of Seq ID No 74; 30-36, 50-56, 96-102, 110-116, 125-131, 162-174, 179-187, 189-201, 223-230, 232-239, 266-278, 320-328, 330-337, 339-350, 388-400, 408-413, 417-423, 435-447, 456-480, 499-524, 526-534, 53-62, 92-107, 192-203, 315-323, 436-452, 464-483, 502-524 and 61-138 of Seq ID No 75; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 126, 174, 225, 267, 309, 316, 320, 337, 436, 466, 467, 473, 474, 14, 128, 143, 228, 347, 494, 2, 52, 112, 201, 209, 217, 230, 235, 236, 337, 381, 395, 413, 419, 454, 466, 510, 515 and 556 of Seq ID No 75; 7-32, 36-56, 77-82, 88-100, 117-144, 153-166, 173-180, 188-226, 256-297, 300-316, 323-337, 339-348, 361-384, 390-427, 438-455, 476-488, 516-523, 535-566, 580-586, 597-607, 615-621, 626-634, 639-649, 654-660, 668-673, 677-688, 707-714, 716-728, 730-742, 746-756, 763-772, 801-808, 820-829, 840-875, 882-888, 895-911, 914-920, 928-948, 953-961, 987-995, 999-1005, 1007-1026, 1053-1060, 1071-1079, 1082-1117, 1123-1129, 6-31, 37-48, 58-69, 90-105, 110-118, 134-142, 146-157, 210-220, 267-276, 291-300, 319-330, 362-372, 393-401, 405-421, 447-456, 463-471, 517-525, 574-582, 597-612, 618-626, 642-650, 656-668, 668-678, 683-695, 725-733, 778-791, 840-849, 894-917, 927-939, 954-963, 966-974, 978-998, 1010-1021, 1056-1067, 1070-1083, 1090-1104 and 325-389 of Seq ID No 76; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 11, 18, 22, 41, 48, 86, 104, 156, 190, 197, 221, 286, 290, 334, 343, 345, 407, 442, 509, 538, 575, 596, 597, 598, 636, 678, 685, 723, 754, 757, 779, 818, 850, 857, 864, 893, 900, 901, 907, 918, 927, 934, 972, 988, 1018, 1025, 1034, 1048, 1065, 1072, 1089, 1094, 1101, 1108, 127, 336, 411, 806, 852, 28, 68, 90, 91, 93, 158, 293, 310, 350, 368, 380, 394, 425, 441, 461, 554, 569, 597, 628, 667, 684, 724, 737, 752, 761, 767, 804, 851, 897, 907, 933, 979, 1030, 1032, 1051, 1075, 1090, 1125, 133, 308, 502, 797, 939 and 960 of Seq ID No 76; 11-19, 34-53, 55-91, 113-119, 122-129, 131-140, 157-170, 173-179, 188-195, 200-206, 208-220, 222-232, 236-244, 250-265, 267-274, 282-290, 293-301, 317-323, 336-343, 355-361, 372-384, 33-54, 69-95, 210-221, 244-254, 257-269 and 324-351 of Seq ID No 77; and fragments with at least 6 amino acid length, preferably

at least 9 amino acid length starting from the position of: 32, 37, 43, 47, 50, 53, 57, 64, 68, 71, 73, 74, 7 80, 82, 113, 120, 155, 162, 194, 205, 209, 231, 235, 238, 252, 259, 266, 273, 280, 287, 294, 301, 308, 315, 333, 16, 18, 66, 377, 36, 44, 81, 99, 124, 193, 261 and 319 of Seq ID No 77; 31-55, 58-64, 69-75, 81-90, 129-150, 15 167, 179-184, 189-208, 227-237, 248-271, 277-284, 313-340, 350-358, 361-368, 371-378, 384-390, 418-425, 43 444, 455-468, 487-506, 514-523, 525-550, 558-569, 572-578, 588-598, 607-618, 645-651, 653-665, 672-684, 70 715, 717-742, 754-771, 776-782, 786-802, 806-817, 1-9, 31-46, 52-61, 60-78, 132-148, 182-199, 214-229, 249-26 280-293, 320-341, 347-355, 386-411, 486-502, 553-575, 624-634, 673-689, 690-700, 702-714, 721-735, 736-74 757-777, 788-798, 810-818 and 90-100 of Seq ID No 78; **and fragments with at least 6 amino acid leng preferably at least 9 amino acid length starting from the position of:** 51, 82, 139, 186, 193, 197, 200, 2 248, 249, 250, 257, 311, 325, 326, 520, 555, 556, 589, 606, 651, 716, 723, 730, 737, 758, 761, 772, 788, 39, 41, 5 695, 709, 783, 51, 60, 89, 110, 141, 207, 216, 295, 301, 395, 404, 518, 527, 555, 568, 593, 596, 673, 691, 722, 7 772, 790, 799, 130, 131, 179, 402, 414 and 701 of Seq ID No 78;13-19, 22-28, 61-67, 74-81, 86-103, 110-1 141-155, 162-169, 171-177, 181-186, 192-199, 201-207, 225-238, 246-263, 273-279, 287-300, 307-313, 331-3 351-367, 370-376, 380-392, 395-402, 415-422, 424-451, 454-465, 473-492, 496-509, 515-523, 541-547, 569-5 589-601, 613-636, 638-647, 653-679, 702-714, 721-729, 739-748, 768-779, 799-813, 821-828, 832-840, 847-8 857-873, 886-892, 894-905, 917-926, 958-971, 974-981, 983-989, 997-1004, 1006-1032, 1034-1049, 1054-10 1063-1069, 1073-1081, 1083-1095, 1097-1115, 1122-1132, 1143-1153, 1164-1171, 1178-1185, 1193-1213, 12 1251, 1258-1272, 1277-1283, 1305-1317, 1324-1330, 1333-1355, 1383-1390, 25-43, 81-92, 111-141, 150-159, 2 220, 222-242, 243-254, 256-267, 276-288, 289-307, 381-397, 398-409, 422-438, 441-464, 485-500, 515-528, 5 553, 569-585, 591-601, 639-649, 656-664, 709-719, 725-734, 739-753, 841-850, 883-893, 902-911, 912-926, 9 948, 960-969, 976-984, 994-1008, 1037-1047, 1073-1085, 1100-1108, 1124-1134, 1167-1179, 1194-1203, 12 1254, 1258-1277, 1308-1319, 1348-1366 and 273-290 of Seq ID No 79; **and fragments with at least 6 ami acid length, preferably at least 9 amino acid length starting from the position of:** 107, 110, 112, 133, 1 200, 204, 223, 244, 251, 271, 289, 291, 305, 323, 360, 380, 407, 422, 428, 440, 491, 507, 512, 536, 616, 625, 6 648, 650, 665, 668, 748, 768, 784, 797, 801, 826, 858, 859, 903, 910, 913, 925, 932, 959, 960, 968, 993, 1008, 1 1068, 1072, 1138, 1141, 1142, 1193, 1201, 1218, 1226, 1237, 1261, 1271, 1311, 1348, 1349, 1377, 126, 375, 4 477, 608, 658, 852, 1106, 1121, 1303, 1362, 24, 102, 151, 164, 169, 211, 229, 245, 274, 279, 285, 333, 348, 3 382, 391, 397, 428, 447, 453, 480, 496, 590, 591, 595, 615, 623, 629, 638, 664, 669, 672, 738, 744, 775, 789, 8 910, 917, 939, 966, 977, 1057, 1084, 1096, 1119, 1127, 1128, 1145, 1163, 1167, 1202, 1214, 1238, 1244, 1 1279, 1335, 145, 355, 961, 1053, 1103 and 1245 of Seq ID No 79; 16-23, 25-47, 49-59, 64-72, 79-91, 95- 113-122, 133-145, 148-162, 169-176, 179-188, 190-200, 202-218, 232-239, 250-283, 299-333, 337-344, 349- 364-406, 430-437, 439-449, 452-460, 464-490, 492-503, 505-530, 533-562, 12-21, 28-39, 52-67, 115-124, 189- 224-232, 234-242, 263-284, 302-322, 363-385, 389-397, 446-463, 479-488, 513-522, 528-552 and 401-419 of ID No 80; **and fragments with at least 6 amino acid length, preferably at least 9 amino acid le starting from the position of:** 23, 30, 58, 78, 84, 97, 98, 120, 123, 133, 162, 169, 189, 215, 218, 236, 309, 316, 365, 372, 384, 388, 391, 426, 446, 453, 465, 466, 478, 508, 513, 515, 523, 530, 536, 543, 554, 333, 467, 13 115, 130, 181, 195, 225, 262, 270, 275, 311, 313, 325, 342, 390, 391, 398, 461, 530, 116, 188 and 229 of Se No 80;8-16, 36-54, 59-76, 85-92, 104-124, 137-180, 199-248, 255-298, 300-307, 324-339, 356-373, 381-393, 442, 448-455, 18-27, 36-56, 101-120, 145-158, 165-173, 179-189, 239-255, 255-270, 330-346, 355-375, 383- 403-421 and 83-232 of Seq ID No 81; **and fragments with at least 6 amino acid length, preferably at 9 amino acid length starting from the position of:** 5, 102, 149, 156, 160, 164, 185, 186, 204, 208, 211, 232, 264, 270, 273, 277, 280, 284, 287, 317, 329, 362, 387, 398, 402, 404, 422, 429, 431, 449, 37, 298, 359, 9 35, 40, 41, 105, 111, 146, 166, 234, 279, 343, 384, 412 and 365 of Seq ID No 81; 29-69, 71-88, 95-104, 106 143-189, 205-232, 24-40, 46-64, 65-79, 83-105, 121-129, 144-199, 206-236 and 182-199 of Seq ID No 82; **fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from position of:** 30, 37, 66, 77, 81, 84, 112, 118, 141, 144, 145, 146, 149, 150, 153, 167, 169, 170, 178, 196, 213, 220, 13, 21, 39, 44, 62, 75, 78, 97, 119, 124, 145, 148, 154, 177, 190, 207, 22 and 216 of Seq ID No 82; 4-46 66, 77-88, 102-110, 115-126, 142-148, 171-181, 183-192, 202-212, 227-234, 251-261, 263-278, 283-316, 319 336-352, 362-371, 386-393, 399-406, 410-425, 427-437, 441-450, 457-464, 471-476, 490-496, 514-521, 549 571-578, 601-611, 618-623, 627-646, 657-670, 672-689, 696-704, 726-740, 742-756, 765-776, 778-784, 792 ~~822-836, 862-868, 875-881, 887-898, 914-919, 941-948, 963-969, 971-978, 996-1004, 1007-1016, 1036-~~ 1068-1080, 1082-1090, 1092-1098, 1104-1127, 1135-1144, 1156-1177, 1181-1195, 1197-1206, 1214-1231,

1263, 1278-1284, 1295-1303, 1305-1323, 1337-1346, 1355-1374, 1376-1383, 1406-1423, 1455-1463, 1465-1489, 1506-1518, 1527-1552, 1555-1570, 1581-1589, 1-28, 109-124, 208-220, 261-280, 286-296, 310-324, 398-405, 425-433, 439-454, 504-517, 535-555, 570-591, 599-614, 620-630, 691-699, 711-719, 729-739, 751-760, 783-791, 843-855, 878-886, 890-900, 940-955, 984-1003, 1007-1026, 1065-1073, 1106-1122, 1136-1149, 1188-1198, 1203-1211, 1227-1235, 1249-1256, 1298-1308, 1374-1392, 1398-1409, 1414-1429, 1436-1444, 1456-1490, 1504-1521, 1530-1547, 1592-1609 and 911-935 of Seq ID No 83; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 26, 33, 79, 170, 200, 265, 290, 297, 302, 304, 333, 334, 377, 412, 414, 415, 431, 436, 458, 465, 481, 494, 536, 546, 568, 605, 678, 690, 697, 703, 724, 729, 730, 735, 737, 767, 776, 797, 840, 861, 938, 968, 999, 1072, 1079, 1085, 1094, 1113, 1160, 1163, 1180, 1188, 1195, 1217, 1245, 1250, 1273, 1302, 1358, 1362, 1363, 1401, 1408, 1465, 1469, 1481, 1507, 178, 960, 1034, 6, 21, 38, 159, 204, 248, 260, 306, 337, 349, 384, 425, 438, 458, 481, 502, 521, 546, 605, 690, 730, 731, 819, 860, 915, 946, 967, 1007, 1018; 1065, 1113, 1187, 1188, 1205, 1223, 1409, 1414, 1495, 1526, 1531, 1537, 101, 255, 1421, 1457, 1538, 1580 and 1589, of Seq ID No 83;15-25, 41-102, 111-117, 127-134, 145-170, 194-201, 207-225, 10-30, 36-44, 46-59, 57-98, 122-138, 144-160, 162-173, 194-217 and 118-131 of Seq ID No 84; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 12, 16, 37, 46, 61, 82, 121, 128, 149, 157, 162, 197, 204, 212, 39, 2, 23, 53, 68, 97, 107, 121, 127, 156, 169, 196, 9, 13 and 114 of Seq ID No 84; 7-54, 65-94, 97-103, 154-163, 170-180, 182-199, 216-222, 227-234, 243-256, 267-273, 286-298, 314-322, 324-353, 363-380, 393-401, 424-431, 434-441, 447-470, 475-495, 506-532, 540-548, 554-592, 594-607, 609-617, 619-626, 628-634, 656-662, 8-31, 43-59, 61-75, 93-104, 126-144, 179-201, 244-254, 289-302, 330-338, 364-382, 413-421, 428-466, 476-525, 582-599, 602-619 621-632 and 115-128 of Seq ID No 85; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 9, 10, 13, 35, 46, 76, 77, 83, 151, 165, 179, 187, 195, 283, 326, 338, 342, 360, 365, 368, 375, 415, 450, 485, 508, 556, 565, 569, 576, 602, 5, 20, 130, 181, 251, 271, 288, 294, 333, 355, 356, 364, 446, 451, 467, 483, 486, 523, 544, 611, 214, 219, 323, 399, 424 and 458, of Seq ID No 85; 5-21, 32-56, 88-99, 117-124, 128-138, 143-150, 168-180, 183-189, 196-213, 220-240, 254-263, 266-289, 300-313, 321-330, 335-358, 361-371, 380-398, 50-65, 67-87, 96-104, 144-153, 156-164, 169-177, 199-220, 259-289, 324-333, 339-360, 372-385 and 74-93 of Seq ID No 86; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 26, 33, 49, 88, 96, 129, 169, 170, 198, 257, 268, 281, 337, 342, 366, 391, 393, 39, 122, 248, 76, 106, 117, 185, 190, 198, 238, 257, 266, 280, 341, 344, 350, 367, 304 and 384 of Seq ID No 86; 12-23, 44-50, 54-60, 91-97, 103-109, 119-125, 131-137, 141-151, 172-183, 201-226, 230-238, 252-265, 315-321, 331-345, 360-370, 376-386, 392-406, 410-416, 422-431, 133-159, 208-222, 354-368 and 1-88 of Seq ID No 87; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 47, 134, 140, 143, 203, 204, 210, 254, 355, 358, 359, 362, 369, 417, 119, 17, 128, 129, 141, 143, 153, 208, 232, 245, 278, 301, 313, 327, 328, 384 and 395 of Seq ID No 87; 4-16, 29-36, 39-64, 69-75, 79-87, 90-122, 126-134, 139-173, 184-190, 195-203, 206-213, 216-228, 234-246, 250-257, 260-266, 274-282, 291-312, 318-325, 340-345, 348-361, 364-388, 399-437, 439-448, 451-464, 467-473, 480-510, 514-520, 534-553, 561-574, 579-589, 593-599, 616-655, 658-671, 3-12, 23-38, 27-38, 43-56, 93-107, 123-137, 144-154, 175-199, 229-244, 288-303, 308-316, 323-337, 410-423, 455-473, 488-496, 531-551, 560-577, 577-591, 619-637, 646-660, 664-672 and 553-570 of Seq ID No 88; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 36, 101, 123, 129, 136, 146, 156, 160, 194, 205, 219, 236, 245, 283, 289, 350, 402, 413, 437, 475, 505, 517, 542, 585, 605, 620, 627, 657, 34, 52, 88, 358, 540, 656, 3, 8, 13, 32, 82, 105, 111, 117, 137, 167, 173, 180, 182, 262, 300, 306, 350, 409, 412, 423, 499, 500, 563, 568, 581, 585, 627, 628, 554 and 638 of Seq ID No 88; 4-31, 50-80, 83-93, 97-103, 111-116, 123-132, 134-163, 170-199, 205-210, 215-220, 230-247, 249-278, 280-308, 311-329, 337-347, 349-358, 365-371, 376-401, 417-430, 434-446, 459-505, 511-518, 527-535, 537-545, 547-565, 573-581, 592-601, 1-17, 20-30, 66-80, 100-119, 139-150, 171-182, 186-198, 207-221, 228-242, 258-274, 286-308, 314-330, 337-352, 355-376, 383-391, 417-432, 437-446, 462-473, 479-488, 496-507, 514-522, 541-554, 557-565, 576-585, 589-605, 49-60 and 582-607 of Seq ID No 89; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 4, 65, 66, 120, 121, 144, 170, 174, 208, 226, 233, 276, 278, 285, 286, 298, 336, 348, 355, 363, 382, 384, 395, 457, 458, 494, 501, 578, 133, 278, 294, 551, 53, 89, 110, 159, 186, 232, 290, 324, 406, 431, 458, 463, 480, 490, 513, 541, 549, 558, 585, 22, 137, 152, 189, 227, 255, 261, 291, 419 and 569 of Seq ID No 89; 9-60, 67-73, 79-93, 109-122, 134-142, 144-153, 165-192, 197-225, 235-244, 259-279, 289-299, 308-317, 321-332, 338-347, 350-361, 373-387, 402-409, 411-421, 439-445,

450-456, 462-468, 470-479, 490-501, 503-516, 16-27, 49-60, 99-122, 136-145, 148-162, 186-194, 213-221, 2: 246, 261-275, 281-292, 353-361, 390-401, 451-470, 486-494, 497-516 and 478-490 of Seq ID No 90; a fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from t position of: 15, 22, 28, 29, 48, 49, 106, 107, 114, 147, 170, 177, 188, 208, 209, 212, 256, 280, 287, 316, 451, 4 489, 33, 217, A03: 36, 98, 124, 136, 142, 153, 177, 188, 251, 262, 291, 320, 323, 383, 417, 464, 487, 491, 492, 5 44, 86, 146, 411, 437 and 499 of Seq ID No 90; 4-10, 16-28, 3-14, 16-30 and 2-16 of Seq ID No 91; a fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from t position of: 1 and15 of Seq ID No 91; 8-18, 20-30 and 7-15 of Seq ID No 92; 4-16, 18-27, 2-13, 20-30 a 10-29 of Seq ID No 93; and fragments with at least 6 amino acid length, preferably at least 9 amino a length starting from the position of: 22 and 1 of Seq ID No 93; 36-57, 62-92, 46-66 and 27-35 of Seq No 94; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starti from the position of: 84 of Seq ID No 94; 4-18, 1-16 and 5-12 of Seq ID No 95; and fragments with least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 1, 9 a 2 of Seq ID No 95; 13-27, 38-52, 1-13, 11-25, 27-37 and 17-36 of Seq ID No 96; and fragments with at le 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 16, 37 and of Seq ID No 96; 4-17, 27-40, 55-62, 9-25, 34-46, 50-64 and 47-62 of Seq ID No 97; and fragments with least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 7, 10, 14 and 58 of Seq ID No 97; 4-9, 1-10 of Seq ID No 98; 3-14 and 7-20 of Seq ID No 99; and fragments w at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 2 1 of Seq ID No 99; 7-12, 24-29, 22-30 and 7-21 of Seq ID No 100; and fragments with at least 6 am acid length, preferably at least 9 amino acid length starting from the position of: 4 and 9 of Seq ID 100; 14-30, 15-30 and 3-18 of Seq ID No 101; and fragments with at least 6 amino acid length, prefera at least 9 amino acid length starting from the position of: 1 and 20 of Seq ID No 101; 3-17 of Seq ID 102; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length start from the position of: 1 of Seq ID No 102; 4-27, 31-59, 75-86, 93-103, 105-110, 15-44, 51-61, 79-95 and 4 of Seq ID No 103; and fragments with at least 6 amino acid length, preferably at least 9 amino length starting from the position of: 11, 15, 24, 28, 31, 35, 36, 42, 48, 49, 53, 78, 79, 97, 20, 28, 35, 37, 43, 60, 65, 77, 85, 86, 21 and 103 of Seq ID No 103; 4-13 and 2-14 of Seq ID No 104; and fragments wit least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 7 an of Seq ID No 104; 4-15, 17-23, 39-52, 4-13, 16-29, 40-50 and 33-41 of Seq ID No 105; and fragments wit least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 3, 3 and 41 of Seq ID No 105; 4-25 of Seq ID No 106; 8-19, 40-47, 67-86, 88-125, 15-25, 48-59, 64-80, 108 and 60-70 of Seq ID No 107; and fragments with at least 6 amino acid length, preferably at lea amino acid length starting from the position of: 7, 110, 16, 34 and 109 of Seq ID No 107; 4-27, 41-46, 30-47 of Seq ID No 108; and fragments with at least 6 amino acid length, preferably at least 9 am acid length starting from the position of: 19, 1 and 23 of Seq ID No 108; 21-28, 34-43, 8-16 and 23- Seq ID No 109; and fragments with at least 6 amino acid length, preferably at least 9 amino acid le starting from the position of: 34, 19, 28 and 39 of Seq ID No 109; 8-20, 24-37, 39-50, 61-67, 69-91, 4-16 42, 84-93 and 42-59 of Seq ID No 110; and fragments with at least 6 amino acid length, preferab least 9 amino acid length starting from the position of: 4, 24, 79, 83, 7, 25, 71, 79 and 91 of Seq ID 110; 4-25, 31-39, 59-97, 100-118, 120-129, 26-40, 49-57, 66-95, 97-128, 131-139, 38-47 of Seq ID No 111; fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from position of: 8, 24, 61, 67, 72, 103, 112, 3, 39, 74, 110 and 119 of Seq ID No 111; 7-24, 32-43, 45-57, 32-48 27-43 of Seq ID No 112; and fragments with at least 6 amino acid length, preferably at least 9 a acid length starting from the position of: 14, 18, 38, 47 and 14 of Seq ID No 112; 4-18, 20-26, 31-37, 33-43 and 34-53 of Seq ID No 113; and fragments with at least 6 amino acid length, preferably at le amino acid length starting from the position of: 3, 7, 10 and 9 of Seq ID No 113; 15-23, 25-39, 43-50 70, 16-32, 61-73 and 67-84 of Seq ID No 114; and fragments with at least 6 amino acid length, prefe at least 9 amino acid length starting from the position of: 8 and 64 of Seq ID No 114; 4-13, 28-42, 28-39 and 1-20 of Seq ID No115; and fragments with at least 6 amino acid length, preferably at le ~~amino acid length starting from the position of: 31, 7 and 5 of Seq ID No115; 4-10, 19-26, 21-29 and~~ of Seq ID No 116; 4-22, 40-46, 51-57, 64-76, 2-10, 45-53, 58-72, 73-82 and 33-45 of Seq ID No117

fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 35, 76, 3, 1 and 66 of Seq ID No117; 12-24, 27-42, 13-30, 34-44 and 1-9 of Seq ID No 118; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 36, 15 and 18 of Seq ID No 118; 4-55, 5-15, 17-33 and 26-45 of Seq ID No 119; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 14 and 53 of Seq ID No 119; 31-42, 45-52, 86-92, 8-16, 35-52, 83-91 and 27-93 of Seq ID No 120; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 86, 56, 21 and 4 of Seq ID No 120; 237 – 256, 508 – 530 of Seq ID No 61; 227 – 239 of Seq ID No 62; 141 – 160, 168 – 187, 155 – 173 of Seq ID No 63; 101 – 124, 161 – 187, 59 – 85, 80 – 106 of Seq ID No 64; 97 – 112 of Seq ID No 66; 139 – 165 of Seq ID No 67; 10 – 21 of Seq ID No 68; 667 – 688, 677 – 696, 161 – 187, 183 – 209, 205 – 231, 226 – 252 of Seq ID No 69; 603 – 629, 622 – 648, 643 – 669 of Seq ID No 70; 529 – 541 of Seq ID No 71; 12 – 34, 29 – 51, 46 – 67, 62 – 83 of Seq ID No 72; 139 – 151 of Seq ID No 73; 246 – 262, 251 – 275 of Seq ID No 74; 61 – 84, 79 – 102, 97 – 120, 115 – 138 of Seq ID No 75; 325 – 350, 345 – 370, 365 – 389 of Seq ID No 76; 324 – 349, 336 – 351 of Seq ID No 77; 90 – 100 of Seq ID No 78; 274 – 290 of Seq ID No 79; 401 – 419 of Seq ID No 80; 84 – 107, 101 – 123, 117 – 139 of Seq ID No 81; 182 – 199 of Seq ID No 82; 911 – 935 of Seq ID No 83; 118 – 131 of Seq ID No 84; 115 – 128 of Seq ID No 85; 74 – 93 of Seq ID No 86; 21 – 43, 54 – 76 of Seq ID No 87; 554 – 570 of Seq ID No 88; 478 – 490 of Seq ID No 90; 2 – 14 of Seq ID No 91; 7 – 15 of Seq ID No 92; 10 – 28 of Seq ID No 93; 27 – 34 of Seq ID No 94; 17 – 35 of Seq ID No 96; 47 – 61 of Seq ID No 97; 1-10 of Seq ID No 98; 7-20 of Seq ID No 99; 7-20 of Seq ID No 100; 3-17 of Seq ID No 101; 3-17 of Seq ID No 102; 41-50 of Seq ID No 103; 2-14 of Seq ID No 104; 33-41 of Seq ID No 105; 4-25 of Seq ID No 106; 60-69 of Seq ID No 107; 23-41 of Seq ID No 109; 42-59 of Seq ID No 110; 38-46 of Seq ID No 111; 27-43 of Seq ID No 112; 34-53 of Seq ID No 113; 67-84 of Seq ID No 114; 1-20 of Seq ID No 115; 33-45 of Seq ID No 117; 26-45 of Seq ID No 119; 27-53 of Seq ID No 120, and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences. Preferred lenghts of the fragments are 6, 7, 8, 9, 10, 11, 12, 20 and 25 amino acid residues. Such fragments are generally easily produceable and can properly be handeled even for bulk production. All these fragments individually and each independently form a preferred selected aspect of the present invention.

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or

fragment thereof according to the present invention. Generally, any vector suitable to mainta propagate or express nucleic acids to express a polypeptide in a host may be used for expression in tl regard. In accordance with this aspect of the invention the vector may_be, for example, a plasmid vect a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starti plasmids disclosed herein are either commercially available, publicly available, or can be construct from available plasmids by routine application of well-known, published procedures. Preferred amo vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune ser reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells c be used in a conventional manner to produce the gene product encoded by the recombinant sequen Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-f translation systems can also be employed to produce such proteins using RNAs derived from the D construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic a molecules of the present invention. Representative examples of appropriate hosts include bacterial c such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtillis* cells; fungal cells, such yeast cells and *Aspergillus* cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal c such as CHO, COS, Hela, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *C. pneumoniae* hyperimmune serum reac antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reac antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invent The invention further provides a process for producing a cell, which expresses a *C. pneumo* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfectir suitable host cell with the vector according to the present invention such that the transforme transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include only secretion signals but also additional heterologous functional regions. Thus, for instance, a regio additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus o polypeptide to improve stability and persistence in the host cell, during purification or du subsequent handling and storage. Also, regions may be added to the polypeptide to facil purification. Such regions may be removed prior to final preparation of the polypeptide. The additic peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facil purification, among others, are familiar and routine techniques in the art. A preferred fusion pr comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypept For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins compr various portions of constant region of immunoglobin molecules together with another protein or thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions fo purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. e 1995} and {Johanson, K. et al., 1995}.

The *C. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof can be recovered purified from recombinant cell cultures by well-known methods including ammonium sulfate or et precipitation, acid extraction, anion or cation exchange chromatography, phosphocell chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and chromatography.

~~The hyperimmune serum reactive antigens and fragments thereof according to the present inventio~~ be produced by chemical synthesis as well as by biotechnological means. The latter compris

transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of a disease related or linked to the presence or abundance of the family of Gram-negative Chlamydiaceae bacteria. More preferably, the microorganisms are selected from the group comprising *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia muridarum*, especially the microorganism is *Chlamydia pneumoniae.*

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm^2 is in a preferred embodiment as little as 10 peptides/polypeptides per cm^2 to at least 400 different peptides/polypeptides per cm^2 and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm^2.

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the

generation of an array as described above. This applies as well to an array made of antibodies, preferak monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmu serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the prese invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimer single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expressi library. It is within the present invention that the antibody may be chimeric, i. e. that different pa thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments ther corresponding to a sequence of the present invention can be obtained by direct injection of hyperimmune serum reactive antigens and fragments thereof into an animal or by administering hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. T antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments ther itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum react antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmu serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmu serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibo produced by continuous cell line cultures can be used (as described originally in {Kohler, G. et al., 197

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) car adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens fragments thereof according to this invention. Also, transgenic mice, or other organisms such as o mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reac antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody g with binding activities towards the hyperimmune serum reactive antigens and fragments thereof ei from repertoires of PCR amplified v-genes of lymphocytes from humans screened for posses respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epito termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum rea antigens and fragments thereof of the present invention by attachment of the antibody to a solid sup for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments th of the present invention may be employed to inhibit and/or treat infections, particularly bac infections and especially infections arising from *C. pneumoniae*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopicall immunologically equivalent derivatives, which form a particular aspect of this invention. The "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive an and fragments thereof or its equivalent which will be specifically recognized by certain antibodies w

when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}; {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18}, preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the

so-called "anticalines" which are, among others, described in German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of t hyperimmune serum reactive antigens and fragments thereof according to the present invention, and method for the manufacture of such functional nucleic acids whereby the method is characterized by t use of the hyperimmune serum reactive antigens and fragments thereof according to the prese invention and the basic steps are known to the one skilled in the art. The functional nucleic acids a preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifica interact with a target molecule. The manufacture or selection of aptamers is, e.g. described in Europe patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of sever preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted w the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increas affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The bindi nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the th obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeat several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding the target from which the final binding nucleic acid is then optionally selected. These specifically bindi nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generati or identification of the aptamers samples of the mixture of individual nucleic acids may be taken determine the sequence thereof using standard techniques. It is within the present invention that aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known the one skilled in the art of generating aptamers. Such modification may for example reside in introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers currently used as therapeutical agents. However, it is also within the present invention that the t selected or generated aptamers may be used for target validation and/or as lead substance for development of medicaments, preferably of medicaments based on small molecules. This is actually d by a competition assay whereby the specific interaction between the target molecule and the aptame inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target aptamer it may be assumed that the respective drug candidate allows a specific inhibition of interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at l in principle, be suitable to block the target and thus decrease its biological availability or activity respective system comprising such target. The thus obtained small molecule may then be subjec further derivatisation and modification to optimise its physical, chemical, biological and/or med characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufactur spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nuc acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers Spiegelmers are characterized by the fact that they have a very high stability in biological systems comparable to aptamers, specifically interact with the target molecule against which they are directe the process of generating spiegelmers, a heterogeonous population of D-nucleic acids is created and population is contacted with the optical antipode of the target molecule, in the present case for exan with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum rea antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic a are separated which do not interact with the optical antipode of the target molecule. But those D-nu acids interacting with the optical antipode of the target molecule are separated, optionally ident and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based o nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids, which identical in terms of sequence with the aforementioned D-nucleic acids interacting with the op

antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA, which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in {Doherty, E. et al., 2001} and {Lewin, A. et al., 2001}.

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybride complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as

more particularly described in the above two mentioned US patents. These oligonucleotides contain n naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotide 2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. Th linkages between the 2'-modified nucleotides can be phosphodiesters, phosphorothioate or I ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activatin region, which contains between 3 and 5 2'-deoxyphosphorothioate nucleotides to activate bacterial RNas H and between 5 and 10 2'- deoxyphosphorothioate nucleotides to activate eucaryotic and, particularl mammalian RNase H. Protection from degradation is accomplished by making the 5' and 3' termin bases highly nuclease resistant and, optionally, by placing a 3' terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5' terminus and a 3' terminus; and fro position 11 to 59 5'→3'-linked nucleotides independently selected from the group consisting of 2 modified phosphodiester nucleotides and 2'-modified P-alkyloxyphosphotriester nucleotides; ar wherein the 5'-terminal nucleoside is attached to an RNase H-activating region of between three and t contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3'-terminus of sa oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguo stretch of one to three phosphorothioate 2'-modified ribonucleotides, a biotin group and a alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5' terminal nucleoside is attached to RNase H-activating region but the 3' terminal nucleoside as specified above. Also, the 5' terminus selected from the particular group rather than the 3' terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof accordi to the present invention may be used as or for the manufacture of pharmaceutical compositio especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the preventi or treatment of diseases caused by, related to or associated with C. *pneumoniae*. In so far another aspect the invention relates to a method for inducing an immunological response in an individual, particularl mammal, which comprises inoculating the individual with the hyperimmune serum reactive antige and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibod to protect said individual from infection, particularly chlamydial infection and most particularly *pneumoniae* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functiona encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a vari thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragmen a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individ from disease, whether that disease is already established within the individual or not. One way administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced in host capable of having induced within it an immunological response, induces an immunological respo in such host, wherein the composition comprises recombinant DNA which codes for and expresses antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. immunological response may be used therapeutically or prophylactically and may take the form antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment the ~~may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabili~~ the first protein and producing a fused protein which will have immunogenic and protective proper

This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *Chlamydia pneumoniae*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *C. pneumoniae* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue and mucosal tissues caused e.g. by viral infection (esp. respiratory, such as the flu) mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or tramsdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *C. pneumoniae*. Such a pharmaceutical composition may comprise one or more hyperimmune serum reactive antigens or fragments thereof against *C. pneumoniae*. Optionally, such *C. pneumoniae* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *C. pneumoniae* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *C. pneumoniae*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *C. pneumoniae*. Optionally, such *C. pneumoniae* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *C. pneumoniae*

and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buff substances, stabilisers or further active ingredients, especially ingredients known in connection pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or coding nucleic acid molecule thereof according to the present invention is an immunostimulato compound for further stimulating the immune response to the given hyperimmune serum-reacti antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulato compound in the pharmaceutical preparation according to the present invention is selected from t group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic aci molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvan Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especia vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/ coding nucleic acid molecules thereof according to the present invention other compounds which a biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least o polycationic peptide. The polycationic compound(s) to be used according to the present invention may any polycationic compound, which shows the characteristic effects according to the WO 97/307 Preferred polycationic compounds are selected from basic polyppetides, organic polycations, ba polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at leas amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine a polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range more than 8, especially more than 20, amino acid residues or mixtures thereof. Other prefer polycations and their pharmaceutical compositions are described in WO 97/30721 (e polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 am acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived fr natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. Th (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/138 Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database un the following internet address:

http://www.bbcm.univ.trieste.it/~tossi/pag2.html

Such host defence peptides or defensives are also a preferred form of the polycationic polymer accord to the present invention. Generally, a compound allowing as an end product activation (or do regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cell used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin der antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorpor herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, prefer from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide, which has the amino acid sequence NH_2-RLAGLLRKGGEKIGEKLKKIGOKIKNFFQKLVPQPE-COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids, which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferablly, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the

invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are nc limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. Th formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner includin for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscula subcutaneous, intranasal, intratracheal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectab composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings ar sutures and aerosols, and may contain appropriate conventional additives, including, for examp preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topic formulations may also contain compatible conventional carriers, for example cream or ointment bas and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % weight of the formulation; more usually they will constitute up to about 80 % by weight of t formulation.

In addition to the therapy described above, the compositions of this invention may be used generally a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue a for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibio prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μg antigen / per kg of bo weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compour of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and k comprising one or more containers filled with one or more of the ingredients of the aforementior compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulat or combination. Associated with such container(s) can be a notice in the form prescribed by governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological produ reflecting approval by the agency of the manufacture, use or sale of the product for hun administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. us the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which caused by, linked or associated with Chlamydiaceae bacteria, more preferably, *C. pneumoniae*. connection therewith it is to be noted that *C. pneumoniae* comprises several strains including th disclosed herein. A disease related, caused or associated with the bacterial infection to be preven and/or treated according to the present invention includes besides others community-acqu pneumoniae, bronchitis, pharyngitis, sinusitis in humans.

In a still further embodiment the present invention is related to a screening method using any of hyperimmune serum reactive antigens or nucleic acids according to the present invention. Scree ~~methods as such are known to the one skilled in the art and can be designed such that an agonist o~~ antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prev

the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its acitivity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see {Okano, H. et al., 1991 OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Bo Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens ar fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according the present invention is its capability to bind to any of its interaction partner or the extent of su capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens ar fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the init physical interaction between a pathogen and mammalian host responsible for sequelae of infection. particular the molecules of the invention may be used: i) in the prevention of adhesion of *C. pneumoniae* mammalian extracellular matrix proteins at mucosal surfaces and on in-dwelling devices or extracellular matrix proteins in wounds; ii) to block bacterial adhesion between mammalian extracellu matrix proteins and bacterial proteins which mediate tissue damage or invasion iii) or lead to evasion immune defense; iv) to block the normal progression of pathogenesis in infections initiated other than the implantation of in-dwelling devices or by other surgical techniques, e.g. through inhibiting nutri acquisition {Brown, J. et al., 2001}.

Each of the DNA coding sequences provided herein may be used in the discovery and development antibacterial compounds. The encoded protein upon expression can be used as a target for the screeni of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infect with Chlamydiaceae, especially *C. pneumoniae*, such as pneumonia.

In a still further aspect the present invention is related to an affinity device such affinity device compri as least a support material and any of the hyperimmune serum reactive antigens and fragments ther according to the present invention, which is attached to the support material. Because of the specificity the hyperimmune serum reactive antigens and fragments thereof according to the present invention their target cells or target molecules or their interaction partners, the hyperimmune serum reac antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kin sample applied to the support material provided that the conditions for binding are met. The sample be a biological or medical sample, including but not limited to, fermentation broth, cell debris, preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, st and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence lis from which further features, embodiments and advantages may be taken. It is to be understood tha present examples are given by way of illustration only and not by way of limitation of the disclosure.

~~In connection with the present invention~~

Figure 1 shows the characterization of *C. pneumoniae* specific human sera.

Figure 2 shows the characterization of the small fragment genomic library, LCPn-50, from *Chlamydia pneumoniae* AR39.

Figure 3 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Table 1 shows the summary of the screens performed with genomic *C. pneumoniae* libraries and human serum.

Table 2 shows the summary of epitope serology analysis with human sera.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera for anti-*C. pneumoniae* antibodies as measured by immunoblotting. Sera were preselected for high anti-*C. pneumoniae* IgG antibody levels by Chlamydien-IgG-ELISA medac. Proteins of the elementary bodies (EB) isolated from *C. pneumoniae* AR39 infected HeLa cells were separated on SDS-PAGE gels and transferred to nitrocellulose membrane. Results of a representative experiment using selected patients' sera at 5.000X dilution are shown. Blots were developed with anti-human IgG secondary antibody reagent. The most reactive samples were selected into screening pools (indicated with *). Mw: molecular weight markers.

Figure 2 (A) shows the fragment size distribution of the *Chlamydia pneumoniae* AR39 small fragment genomic library, LCPn-50. After sequencing 480 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. **(B)** shows the graphic illustration of the distribution of the same set of randomly sequenced clones of LCPn-50 over the *C. pneumoniae* chromosome (according to the AR39 genome data). Rectangles indicate matching sequences to annotated ORFs and diamonds represent fully matched clones to non-coding chromosomal sequences in +/+ or +/- orientation, respectively. Circles position all clones with chimeric sequences. Numeric distances in base pairs are indicated over the circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 (A) shows the MACS selection with biotinylated human IgGs. The LCPn-50 library in pMAL9.1 was screened with 10 to 20 μg biotinylated IgG (P14-IgG, purified from human serum). As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st and/or 2nd elution are shown for each of the three selection rounds. **(B)** shows the reactivity of specific clones (1-25) selected by bacterial surface display as analysed by immunoblot analysis with the human serum IgG pool (P14-IgG, 4μg/μl) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000 of immune rabbit serum.

Table 1: Immunogenic proteins identified by bacterial surface display.
A, 50bp library (LCPn-50) of *C. pneumoniae* AR39 in *lamB* with **P14-IgG** (number of clones after trimming: 755), B, 300bp library (LCPn-300) in *fhuA* with **P14-IgG** (669); The number of selected clones per ORF is listed as well as the immunogenic region delineated by the selected clones. CP0018, annotated reading frame of C. pneumoniae; ARF0217, predicted novel ORF in alternative reading frame of CP0217; CRF0014, predicted novel ORF on complement reading frame of CP0014. *, prediction of sequences longer than 5 amino acids capable of inducing an antibody response was performed with the program ANTIGENIC {Kolaskar, A. et al., 1990}; **, prediction of sequences capable of inducing a class II-restricted

T cell response was performed with the program TEPITOPE {Bian, H. et al., 2003}. Epitopes or regions a shown that are identified in at least four of the eigth MHC types analysed with a threshold of 5%. * prediction of nonameric sequences capable of inducing a class I-restricted T cell response was perform with the program SYFPEITHI {Rammensee, H. et al., 1999}. Epitopes are shown that are identifi individually for four MHC types (A0201, B0702, A03, A2402) with a score above 20.

Table 2: Epitope serology with human sera.
Immune reactivity of individual synthetic peptides representing selected epitopes with human se strongly reactive against C. *pneumoniae* is shown. The extent of reactivity is expressed as scores, wh were calculated based on the sum of ELISA reactivities with 22 individual sera, based on the followi calculations: - =0; + =1; ++ =2; +++ =3. Positivity was assessed based on OD_{405nm} readings at two differ serum dilutions after correction for background. Locations of synthetic peptides within the antige ORFs according to the genome annotation of the C. *pneumoniae* AR39 strain are given in the 2nd colu indicating the first and last amino acid residue, respectively. Peptide names: CP0018.1, present annotated CP0018; ARF0271.1, present in potential novel ORF in alternative reading-frame of CP02 CRF1083.1, present in potential novel ORF on complement of CP1083.

EXAMPLES

Example 1: Characterization and selection of human sera based anti-C. *pneumoniae* antibod preparation of antibody screening reagents.

Experimental procedures

Enzyme linked immune assay (ELISA).
A commercially available ELISA kit, Chlamydien-IgG-ELISA medac (Medac Gmbh, Germany), wh employes a highly purified and specific antigen was used to measure anti-C. *pneumoniae* antibody tit Three dilutions of sera, 400X, 200X, 100X were tested, and reactivities were expressed as titers > 1: 1:400; 1:200; 1:100 and <1:100.

Immunoblotting
Elementary bodies (EB), used as bacterial antigen extract were isolated from C. *pneumoniae* AR39 infe HeLa cell cultures according to {Wang, S. et al., 1991}. The infectivity of EBs was destroyed and prot were solubilized by adding SDS-PAGE sample buffer containing SDS and 2-mercaptoetha Approximately 5μg total protein was separated by SDS-PAGE using the BioRad Mini-Protean 3 electrophoresis system and proteins were transferred to nitrocellulose membrane (ECL, Amers Pharmacia). After overnight blocking in 5% milk, human sera were added at 5,000x dilution, and H labeled anti-human IgG was used for detection.

Purification of antibodies for genomic screening. Five sera were selected based on the overall anti-chlamy titers for a serum pool used in the screening procedure. Antibodies against *E. coli* proteins were rem by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pH grown under the same condition as used for bacterial surface display). Highly enriched preparatio IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, accordi the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). The efficiency of purification was checked by SDS-PAGE and protein concentration measurements (OD_{280nm}).

Results
The antibodies produced against C. *pneumoniae* by the human immune system and present in huma ~~are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity.~~ T molecules are essential for the identification of individual antigens in the approach as described i

present invention, which is based on the interaction of the specific anti-chlamydial antibodies and the corresponding *C. pneumoniae* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from patients with symptoms of *C. pneumoniae* related infections, such as pneumonia, and bronchitis. *C. pneumoniae* was indicated to be the causative agent by medical serological tests.

Infections with *Chlamydia pneumoniae* are detected and diagnosed by serology, since the pathogen is not culturable with routine microbiological methods. Highly specific and sensitive diagnostic kits based on antigen detection have been developed and are available commercially. We have selected patients' sera having a high titer against *C. pneumoniae* detected by a standard Chlamydia ELISA kit routinely used in the clinic for diagnosis of acute, chronic and persistent infections caused by Chlamydia species. 185 serum samples were tested, all derived from individuals selected for diagnostic testing for the presence of *Chlamydia pneumoniae* specific antibodies based on clinical symptoms. 83 sera showed antibody titers > 1:400; 34 sera showed titers of approximately 1:400; 14 sera of 1:200; 20 sera of 1:100 and 34 sera had titers < 1:100. According to epidemiologic studies *C. pneumoniae* carriage and infection is widespread, with frequent reinfection during lifetime. For that reason, primary selection of sera aimed at the identification of samples with the highest IgG titer (> 400) to reduce the risk of nonspecific, false positive diagnosis.

Subsequently, pre-selected sera were analysed by immunoblotting to ensure antibody reactivities against multiple proteinaceous antigens present in *C. pneumoniae*. The representative immunblot shown in Fig. 1 demonstrates that different patterns of reactivities were detected with the individual sera when tested against proteins of elementary bodies, isolated from infected human cells (HeLa) in *in vitro* cultures. Special attention was made to select sera displaying different pattern of reactivities based on these immunoblot analysis.

Five selected sera were pooled to further enrich for abundant antibodies, but still having a representation of antibody repertoires of different individuals. IgG antibodies were purified from pooled sera by affinity chromatography and depleted of *E. coli* -reactive antibodies to avoid background in the bacterial surface display screen.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Chlamydia pneumoniae* AR39.

Experimental procedures

Preparation of chlamydial genomic DNA. *C. pneumoniae* AR39 was cultivated as described in {Campbell, L. et al., 1989}. Elementary bodies (EB) were isolated and used for the preparation of genomic DNA. Genomic DNA from *C. pneumoniae* EBs was prepared as described by {Cox, R. et al., 1988}. The final genomic DNA preparation was dissolved in ddH_2O.

Preparation of small genomic DNA fragments. Genomic DNA from *C. pneumoniae* AR39 was mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DNase I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DNase I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DNase I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total

fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twi using T4 DNA Polymerase in the presence of 100 μM each of dNTPs to ensure efficient flushing of tl ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone {Skerra, A 1994} with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition tl *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasm membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature bet lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after tl leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region wou decrease or abolish translocation across the cytoplasmic membrane {Kajava, A. et al., 2000}. A *Sm* restriction site serves for library insertion. An upstream FseI site and a downstream NotI site, which we used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted aft the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pE {Hashemzadeh-Bonehi, L. et al., 1998}. Subsequently, a sequence was inserted in *lamB* after amino a 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion w constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with F and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pE Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, X and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected D fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous read frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic *C. pneumoniae* AR39 DNA fragments w ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented w Kanamycin (50 μg/ml) and Ampicillin (50 μg/ml). Plates were incubated over night at 37°C and colo collected for large scale DNA extraction. A representative plate was stored and saved for collect colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was use initially determine the rough fragment size distribution as well as insertion efficiency. From sequen data the precise fragment size was evaluated, junction intactness at the insertion site as well as the fr selection accuracy (*3n+1 rule*).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised f the pMAL4.31 vector, containing the *C. pneumoniae* library with the restriction enzymes *Fse*I and *Not*I. entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (Fh which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in ea the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells electroporation. Cells were plated onto large LB-agar plates supplemented with 50 μg/ml Kanamycin grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scrape the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening 80°C.

Results

Libraries for frame selection. Two libraries (LCPn-50 and LCPn-300) were generated in the pMAL4.31 vector with sizes of approximately 50 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *C. pneumoniae* AR39 DNA yielded 6x 10^4 to 3x 10^5 clones after frame selection. To assess the randomness of the libraries, 480 randomly chosen clones of LCPn-50 were sequenced. After trimming of the vector sequences, 390 could be subjected to bioinformatic analysis, showing that of these clones only very few were present more than once. Furthermore, it was shown that 98% of the clones fell in the size range between 25 and 100 bp with an average size of 46 bp (Figure 2). Allmost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LCPn libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *Fse*I and *Not*I restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in 2x 10^5 to 2x 10^6 clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *C. pneumoniae* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5x 10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2x 10^7 cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

Ten to 20 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated overnight at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (For IgA screens, 10 to 20 µg of purified IgAs were used and these captured with biotinylated anti-human-IgG secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 µg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min. Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 µl LB medium. 10 µg of human, biotinylated IgGs were added again and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were either subjected to a third round of selection or plated onto LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown overnight 37°C in 3 ml LB medium supplemented with 50 μg/ml Kanamycin to prepare plasmid DNA usi standard procedures. Sequencing was performed at MWG (Germany).

For Western blot analysis approximately 10 to 20 μg of total cellular protein was separated by 10% SD PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB FhuA fusion proteins were detected using human serum as the primary antibody at a dilution approximately 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharma Biotech, England). Alternatively, rabbit anti-FhuA or rabbit anti-LamB polyclonal immune sera we used as primary antibodies in combination with the respective secondary antibodies coupled to HRP f the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated I The libraries LCPn-50 in pMAL9.1 and LCPn-300 in pHIE11 were screened with a pool of biotinylat human IgGs from patient sera (see Example 1: *Preparation of antibodies from human serum*). The selecti procedure was performed as described under Experimental procedures. Figure 3A shows the d obtained with the screen of the LCPn-50 library and P14-IgGs. As can be seen from the colony count af the first selection cycle from MACS screening, the total number of cells recovered at the end is drastica reduced from 1x10^7 cells to approximately 6x 10^4 cells, but the selection without antibodies added show a similar reduction to a number of about 5x10^3 cells (Figure 3A). After the second round, a simi number of cells was recovered with P14-IgGs, while only 7x 10^3 cells were recovered when no IgGs fr human serum were added, clearly showing that selection was dependent on *C. pneumoniae* spec antibodies. The third round reduced the number of cells in the sample with P14-IgGs and without I added, but it is clearly obvious that selection of cells was specific for the *C. pneumoniae* antibodies pres in the human serum applied for the screen. To evaluate the performance of the screen, 25 selected clo were picked randomly and subjected to immunoblot analysis with the screening IgG pool (P14-I (Figure 3B). This analysis revealed that more than 90% of the selected clones showed reactivity w antibodies present in the relevant serum, whereas the control strain expressing LamB without a *pneumoniae* specific insert did not react with the same serum (not shown). In general, the rate of reacti was observed to lie within the range of 35 to 95%. Colony PCR analysis showed that all selected clo contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 800 per screen) led to identification of the gene and the corresponding peptide or protein sequence that was specific recognized by the human serum antibodies used for screening. The frequency with which a specific cl is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the se used for selection and recognizing the epitope presented by this clone. In that regard it is striking clones derived from some ORFs (e.g. CP0051, CP0070) were picked very frequently (40 to 200 tim indicating their highly immunogenic property. Table 1 summarizes the data obtained for the performed screens. All clones that are presented in Table 1 have been verified by immunoblot anal using whole cellular extracts from single clones to show the indicated reactivity with the pool of hu serum used in the respective screen. As can be seen from Table 1, distinct regions of the identified are identified as immunogenic, since variably sized fragments of the proteins are displayed on the su by the platform proteins.

It is further worth noticing that a large number of the genes identified by the bacterial surface dis screen encode proteins of *C. pneumoniae*, which have no assigned function or may even const proteins, which have not been predicted by previous bioinformatic analsis. Thus, many of t candidates constitute novel antigenic proteins of *C. pneumoniae*.

Example 4: Assessment of the reactivity of highly immunogenic peptide sequences with individual human sera.

Experimental procedures

Peptide synthesis

Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (Multisyntech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-aminohexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93%TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

Enzyme linked immune assay (ELISA).

Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates at 10 µg/ml concentration. Strepatavidin plates were prepared by coating with Streptavidin (Sigma) at 5 µg/ml concentration overnight. Human sera were tested at two serum dilutions, 200X and 1,000X. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

Results

Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed with 20 selected highest titer sera - among those the ones included in screening pools - and with two negative controls, having lower titers according to ELISA. A summary for serum reactivity of 80 peptides representing 58 *C. pneumoniae* antigens identified in the genomic screens is shown in Table 2. The 80 peptides represent 29 ORFs, 13 ARFs and 16 CRFs. The peptides were compared by the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Extent of reactivity was expressed as scores, which were calculated based on the sum of ELISA reactivities with 22 individual sera, based on the following calculations: - =0; + =1; ++ =2; +++ =3. Positivity was assessed based on OD_{405nm} readings at two different serum dilutions after correction for background. Peptides ranged from highly and widely reactive to weakly positive ones. The highest possible score, 122, would belong to a peptide, which displays +++ reactivity with all 22 sera at both 200X and 1000X serum dilutions (3x22x2=122). Among the most reactive ones with scores greater than 20, there are alternative and complementary strand antigens (ARF1062 and CRF0016, CRF1073), as well as epitopes present in annotated ORFs (CP0161, CP0282, CP0316, CP0426, CP0693 and CP0737). The lower scoring peptides were mainly reactive with the sera used for their identification, but did not show wide reactivity with other serum samples.

These data suggest that individual patients infected with *C. pneumoniae* recognize different patterns of antigens and different antigenic epitopes within the antigens. However, there is a substantial overlap among the antigen specificities of anti-*C. pneumoniae* antibody repertoires of individual patients against certain epitopes identified by the method of the present invention examplified by the identification of

high scoring peptides.

Example 5: Identification of HLA class I-restricted and HLA class II-restricted T cell epitopes epitope regions within the selected antigens.

Experimental procedures

HLA class I-restricted epitope prediction

The prediction of HLA class I-restricted epitopes within the antigen identified by bacterial display w performed using the program SYFPEITHI as described by {Rammensee, H. et al., 1999}.

(http://syfpeithi.bmi-heidelberg.com/Scripts/MHCServer.dll/EpPredict.htm)

The prediction was performed for the four MHC types HLA*A0201, B0702, A03 and A2402. For all four MHC types, only predicted epitopes of a length of 9 amino acids with a score above 20 are listed.

HLA class II-restricted epitope prediction

The prediction of HLA class II-restricted epitopes within the antigen identified by bacterial display w performed using the program TEPITOPE as described by {Bian, H. et al., 2003}. The prediction w performed for the eight MHC types DRB1*0101, 0301, 0401, 0701, 0801, 1101, 1501 and DRB*0101. For predictions, those epitopes or regions are listed, which showed a hit with a threshold of 5% for at leas MHC types. The listed epitopes or regions are selected in such a way that a region as small as possib but in any case smaller than 25 amino acids contains a hit in at least 4 MHC types. Only in cases wh epitopes overlap continuously in a larger region, the whole region (potentially larger than 25 ami acids) is depicted.

Results

T cell epitopes are the minimal essential units of information derived from nonself (or self) proteins tha stimulate cellular (T cell) immune responses. They are presented in the cleft of MHC class I or class II molecules at the surface of the antigen-presenting cell to the T cell receptor (TCR). The following casca of cellular events triggered by the interaction of a TCR and the pathogen-derived peptide epitope in th cleft of an MHC molecule serves to inform the cellular immune system that bacteria, viruses or parasit are present. Induction of epitope-specific T cell responses may improve immune responses to pathoge for which no convential vaccines currently exist and thus provide a means to allow protection from infection or to clear an infection by the respective pathogen. The accuracy of the bioinformatic predicti methods for T cell epitopes are remarkable {Martin, W. et al., 2003} and thus offer a complementary method to the described antigen identification approach by bacterial surface display, which is based o the experimental identification on B cell epitopes. Since the ORFs, corresponding to the antigens identified on the basis of recognition by antibodies in human sera, most likely also contain linear T-cel epitopes it was the aim of this invention to provide also a set of T cell epitopes for the listed antigens.

The molecular definition of the corresponding HLA class II helper-epitopes is usefull for the design of synthetic anti-chlamydial vaccines, which can induce immunological memory, because the helper-epitopes derived from the chlamydial antigens provide "cognate help" to the B-cell response against th antigens or fragments thereof. Moreover it is possible to use these helper-epitopes to induce memory T-independent antigens like for instance carbohydrates (conjugate vaccines). MHC class II molecules peptides consisting of 11 to 25 amino acids and are predominantly recognized by CD4+ helper T cells. is evident from Table 1, almost all antigens identified by bacterial surface display contain a number o potential MHC class II-restricted epitopes, which may also overlap with the identified B cell epitopes CP0426).

More importantly, intracellular *Chlamydia pneumoniae* can be eliminated by CD8+ cytotoxic T-cells, which recognize HLA class I-restricted epitopes. MHC class I molecules present in general peptides of 8 to 10 amino acids in length with two conserved anchor residues. The four assessed MHC types as listed in Table 1 comprise approximately 70% of all MHC types in individuals worldwide, so that the occurrence of epitopes within an antigen for these four MHC types provides a broad coverage. While most of the identified antigens belonging to annotated ORFs contain epitopes for all four MHC types (e.g. CP0134, CP0578), only one of the in general much shorter putative novel ORFs (CRF1083), which were not previously annotated, contains epitopes for all four MHC types, but a number of them possesses epitopes for at least 2 or 3 MHC types (e.g. ARF1071, CRF0551). In the context of a protective immune response, epitope-specific T cells can persist as memory cells, thus allowing a more rapid response to the pathogen upon encounter. Therefore and since the two types of cellular immune response are complementary, preventive as well as therapeutic vaccines should be designed to contain both class I-restricted and class II-restricted epitopes.

The identified peptides or fragments thereof (for instance overlapping 15-mers) can be synthesized and tested for their ability to bind to various MHC molecules *in vitro*. Their immunogenicity can be tested by assessing the peptide (antigen)-driven proliferation (BrdU or 3H-thymidine incorporation) or the secretion of cytokines (ELIspot, intracellular cytokine staining) of T-cells *in vitro* ({Schmittel, A. et al., 2000}; {Sester, M. et al., 2000}). In this regard it will be interesting to determine quantitative and qualitative differences in the T-cell response to the chlamydial antigens or the selected promiscuous peptides or fragments thereof e.g. in populations of patients with different chlamydial infections, or in colonized versus healthy individuals neither recently infected nor colonized. In addition, the immunogenicity of the predicted peptides can be tested in HLA-transgenic mice {Sonderstrup, G. et al., 1999}.

Furthermore, the antigens/epitopes may be injected into mice and the induced antibodies and T cells responses can then be determined. The protective capacity of the antibodies and T cells induced by the antigens through vaccination can be assessed in animal models. All these approaches are well available to the skilled man in the art.

Table 1: Immunogenic proteins identified by bacterial surface display.

A, 50bp library of *C.pneumoniae* AR39 in lamB with P14-IgG (755), B, 300bp library in fhuA with P14-Ig (669); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)
CP0018	conserved hypothetical protein	18-29,60-78,89-95,100-105,124-143,166-180,187-194,196-208,224-242,285-294,305-311,313-320,351-360,368-373,390-403,411-429,432-470,483-489,513-523,535-543,548-564,579-587,589-598,604-612,622-627,632-648	55-84, 190-207, 323-331, 370-390, 551-570, 606-614, 633-647	A0201: 60, 63, 67, 70, 126, 129, 133, 136, 169, 186, 200, 308, 371, 414, 421, 434, 444, 459, 503, 512, 532, 540, 547, 601, 625, 632, 634, 637 B0702: 99, 529 A03: 25, 38, 59, 155, 278, 285, 412, 420, 441, 451, 457, 481, 506, 510, 524, 536, 539, 554, 578, 596, 638 A2402: 179, 604	A:4, B:18	39-129, 224-296, 464-609
CP0051	major outer membrane protein, MOMP	4-29,31-38,46-64,66-80,109-115,131-139,152-160,170-183,198-234,239-255,267-290,301-313,318-324,336-345,350-365,380-386	65-82, 123-165, 268-290, 299-307, 320-329, 336-347	A0201: 4, 13, 69, 93, 149, 174, 273, 277, 298, 305, 312, 319, 375 B0702: 28, 303 A03: 3, 58, 73, 100, 153, 191, 223, 227, 232, 251, 269, 286, 343, 374 A2402: 238	A:40, B:3	76-103, 226-239, 267-333
CP0069	hypothetical protein	20-33,35-43,47-60,77-92,113-124,137-145,185-196	66-75	A0201: 32, 48, 49, 113 B0702: 77, 118, 139, 185 A03: 2, 24, 120 A2402: none	A:14, B:19	92-214

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
CP0070	hypothetical protein	47-64,137-155,157-167,182-198,212-233,247-259,291-303,315-337,345-350,355-368,373-379	58-72, 183-196, 249-261, 315-323, 334-342, 347-356, 358-366	A0201: 135, 160, 183, 184, 204, 249, 256, 293, 296, 318, 319, 356, 372 B0702: 94 A03: 13, 60, 159, 163, 189, 204, 220, 233, 300, 333, 335, 356, 362 A2402: 198, 289	A:14, B:187	6-188	4, 64
CP0134	Protease IV, putative	4-36, 43-49, 60-75, 96-107, 113-123, 132-172, 186-193, 217-229, 231-250, 260-282, 284-290, 298-312, 315-330	5-38, 67-77, 113-127, 134-145, 147-156, 220-236, 271-283, 285-293, 296-304, 309-321	A0201: 3, 10, 14, 17, 24, 46, 59, 133, 155, 220, 270, 312 B0702: 233 A03: 2, 22, 31, 36, 62, 65, 122, 140, 155, 162, 170, 189, 235, 248, 260, 286, 298 A2402: 156, 183, 325	B:13	159-217	5, 65
CP0161	conserved hypothetical protein	5-26,29-50,52-61,65-74,89-96,140-147,153-162,183-188,191-197,203-210,213-225	1-9, 30-38, 53-63, 70-78, 92-107, 141-149, 158-166, 174-191, 205-224	A0201: 31, 33, 39, 56, 63, 78, 119, 136, 196 B0702: none A03: 14, 35, 38, 55, 97, 98, 146, 156, 158, 215 A2402: 88, 214	A:4	97-113	6, 66
CP0177	hypothetical protein	31-36,46-54,65-80,86-102,168-175,179-186,188-194,200-208,210-216,225-231,243-257,289-296,362-387,460-474,476-486,504-511,518-525,569-579,581-600,665-	182-193, 202-211, 279-294, 311-319, 369-377, 468-476, 547-558, 579-587, 681-700, 731-740	A0201: 28, 78, 285, 309, 321, 376, 379, 388, 468, 475, 479, 500, 571, 624, 668, 716 B0702: 360, 455, 669 A03: 185, 190, 204, 264, 281, 292, 478, 502, 588, 675, 680, 716, 730 A2402: none	A:2, B:6	92-177, 591-604	7, 67

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	
		684,688-694,700-705,717-735					
CP0254	prolyl-tRNA synthetase	4-9,17-24,27-52,66-77,91-98,104-124,127-139,178-199,211-219,221-228,234-244,246-255,263-286,303-312,316-321,337-346,356-362,367-372,377-390,402-416,449-459,465-479,491-501,503-508,523-541,551-558,560-565	31-69, 115-127, 132-143, 145-165, 176-187, 190-204, 212-220, 266-286, 304-316, 403-423, 440-456, 523-544	**A0201:** 17, 24, 31, 45, 53, 56, 63, 69, 107, 129, 150, 171, 178, 189, 191, 217, 255, 273, 277, 305, 312, 451, 458, 470, 478, 506, 522 **B0702:** 71, 379 **A03:** 20, 29, 34, 44, 119, 133, 276, 284, 300, 328, 404, 465, 470, 529, 543 **A2402:** 182, 551	A:7	9-22	8,
CP0282	hypothetical protein	34-42,52-63,71-87,112-120,142-147,154-159,166-177,180-197,204-224,237-256,260-268,280-286,312-324,338-343,372-412,456-463,479-490,494-504,506-512,518-524,538-548,562-573,585-591,597-606,674-690,703-712,714-740,749-766	95-103, 114-123, 180-195, 205-220, 240-248, 370-400, 481-495, 588-596, 707-715, 750-765	**A0201:** 179, 206, 209, 213, 216, 255, 286, 300, 304, 324, 365, 369, 373, 376, 377, 380, 381, 384, 562, 694, 720, 721, 729, 749, 752, 755 **B0702:** 197, 330, 559, 592, 600, 714, 751 **A03:** 91, 111, 140, 167, 191, 315, 388, 393, 402, 458, 463, 587, 720, 762 **A2402:** 748	A:4, B:4	160-253, 630-717	

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
CP0286	polymorphic membrane protein, E/F family	4-44,50-55,59-67,73-83,91-98,101-109,131-145,230-236,267-273,293-300,303-310,349-354,375-397,404-416,434-441,445-452,456-468,479-485,487-512,544-568,571-579,593-599,604-610,614-621,642-656,665-678,706-716,729-736,748-756,780-795,797-814,827-844,850-861,864-882,889-900,906-933	6-23, 28-36, 64-75, 134-150, 182-192, 227-236, 306-316, 340-350, 376-387, 421-435, 449-460, 527-535, 553-569, 587-595, 641-657, 668-676, 683-694, 743-755, 800-819, 843-865, 861-886, 894-915, 929-938	A0201: 7, 8, 15, 73, 80, 133, 134, 138, 182, 194, 271, 272, 298, 432, 438, 457, 458, 487, 490, 527, 548, 568, 616, 644, 647, 667, 741, 782, 801, 829, 866 B0702: 126, 259, 792 A03: 15, 20, 133, 155, 160, 232, 299, 458, 464, 552, 558, 560, 605, 607, 654, 670, 672, 768, 810, 840, 852, 877, 900 A2402: 167, 380, 425, 593, 907	B:3	603-669	10, 70
CP0306	polymorphic membrane protein, G family	4-32,73-82,90-101,116-132,144-160,171-182,195-200,227-234,255-271,293-300,313-336,344-350,369-375,381-398,413-421,436-465,487-496,503-508,510-527,538-546,552-562,608-614,617-636,663-	7-16, 90-107, 110-137, 170-187, 197-213, 233-251, 277-287, 291-314, 361-390, 412-425, 451-465, 489-498, 513-521, 570-580, 619-637, 662-679, 713-721, 725-733, 745-754, 766-781, 790-805, 817-834, 868-883, 888-903	A0201: 8, 23, 53, 57, 128, 169, 178, 239, 263, 290, 297, 310, 324, 331, 339, 365, 398, 436, 443, 450, 470, 485, 488, 513, 514, 520, 614, 669, 711, 723, 771, 824, 849, 895 B0702: 316, 861 A03: 118, 135, 196, 225, 284, 290, 370, 454, 489, 492, 521, 557, 624, 632, 745, 778, 783, 850, 868, 910	A:7	529-542	11, 71

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	S : (D P:
		674,679-691,705-730,734-748,769-807,825-834,848-861,864-871,891-902		A2402: 226, 383			
CP0316	ATP-dependent Clp protease, ATP-binding subunit	10-18,30-52,63-70,72-79,96-133,146-158,168-175,184-193,203-210,213-222,227-234,237-257,263-273,285-291,297-312,320-338,359-378,385-393,395-410,412-421,490-510,521-527,540-548,563-571,573-585,592-598,615-620,632-641,652-661,672-679,704-711,717-723,729-736,742-751,766-778,788-808,817-824,836-842	34-56, 73-89, 103-130, 146-154, 184-205, 213-227, 245-257, 258-278, 292-316, 331-341, 358-369, 372-383, 388-397, 410-418, 503-514, 524-530, 548-556, 565-573, 584-595, 637-646, 656-663, 673-686, 734-742, 745-754, 757-768, 770-781, 816-828	A0201: 27, 32, 36, 65, 109, 112, 120, 127, 186, 249, 250, 262, 267, 297, 301, 353, 360, 367, 410, 418, 436, 465, 472, 505, 518, 522, 565, 576, 585, 638, 645, 650, 676, 687, 724, 745, 756, 763, 795 B0702: 164, 411, 510, 560, 569, 647, 766, 780 A03: 14, 39, 48, 65, 74, 129, 175, 215, 217, 229, 230, 240, 253, 257, 262, 269, 308, 317, 322, 327, 352, 371, 372, 373, 374, 417, 443, 454, 472, 514, 525, 567, 629, 637, 657, 662, 683, 698, 731, 744, 752, 763, 769, 787, 790, 802, 815, 819 A2402: 26, 102, 381, 704	B:3	14-101	12
CP0339	conserved hypothetical protein	4-14,20-33,36-63,71-93,96-104,106-117,120-128,131-147,161-172,174-186,195-210,212-247,269-286,288-301,306-	35-66, 70-85, 107-118, 124-132, 165-179, 186-196, 197-205, 276-289, 292-300, 348-368, 369-381, 385-394	A0201: 34, 41, 50, 53, 109, 127, 134, 153, 165, 271, 286, 297, 340, 384 B0702: 80, 321, 334, 354 A03: 33, 57, 110, 153, 178, 276, 284, 383	A:2	139-151	

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		322,324-332,348-354,356-363,384-391		**A2402:** 79, 99, 123			
CP0353	A/G-specific adenine glycosylase	12-20,37-48,51-58,69-75,86-98,113-136,141-161,171-216,222-254,264-273,291-301,311-345,351-361	31-39, 40-55, 62-74, 121-137, 148-164, 170-178, 223-253, 309-329, 354-369	**A0201:** 46, 95, 103, 110, 143, 156, 178, 186, 190, 236, 242, 244, 291, 294, 315, 333, 353 **B0702:** 125, 183, 256, 326 **A03:** 3, 68, 82, 102, 131, 177, 185, 190, 193, 223, 224, 244, 250, 295, 340, 349, 354 **A2402:** 88, 89	A:7	246-275	14, 74
CP0426	conserved hypothetical protein	30-36,50-56,96-102,110-116,125-131,162-174,179-187,189-201,223-230,232-239,266-278,320-328,330-337,339-350,388-400,408-413,417-423,435-447,456-480,499-524,526-534	53-62, 92-107, 192-203, 315-323, 436-452, 464-483, 502-524	**A0201:** 126, 174, 225, 267, 309, 316, 320, 337, 436, 466, 467, 473, 474 **B0702:** 14, 128, 143, 228, 347, 494 **A03:** 2, 52, 112, 201, 209, 217, 230, 235, 236, 337, 381, 395, 413, 419, 454, 466, 510, 515, 556 **A2402:** none	B:2	61-138	15, 75
CP0578	conserved hypothetical protein	7-32,36-56,77-82,88-100,117-144,153-166,173-180,188-226,256-297,300-316,323-337,339-348,361-384,390-427,438-455,476-488,516-523,535-566,580-586,597-	6-31, 37-48, 58-69, 90-105, 110-118, 134-142, 146-157, 210-220, 267-276, 291-300, 319-330, 362-372, 393-401, 405-421, 447-456, 463-471, 517-525, 574-582, 597-612, 618-626, 642-650,	**A0201:** 11, 18, 22, 41, 48, 86, 104, 156, 190, 197, 221, 286, 290, 334, 343, 345, 407, 442, 509, 538, 575, 596, 597, 598, 636, 678, 685, 723, 754, 757, 779, 818, 850, 857, 864, 893, 900, 901, 907, 918, 927, 934, 972, 988, 1018, 1025, 1034, 1048, 1065, 1072,	B:5	325-389	16, 76

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	S (D P
		607,615-621,626-634,639-649,654-660,668-673,677-688,707-714,716-728,730-742,746-756,763-772,801-808,820-829,840-875,882-888,895-911,914-920,928-948,953-961,987-995,999-1005,1007-1026,1053-1060,1071-1079,1082-1117,1123-1129	656-668, 668-678, 683-695, 725-733, 778-791, 840-849, 894-917, 927-939, 954-963, 966-974, 978-998, 1010-1021, 1056-1067, 1070-1083, 1090-1104	1089, 1094, 1101, 1108 B0702: 127, 336, 411, 806, 852 A03: 28, 68, 90, 91, 93, 158, 293, 310, 350, 368, 380, 394, 425, 441, 461, 554, 569, 597, 628, 667, 684, 724, 737, 752, 761, 767, 804, 851, 897, 907, 933, 979, 1030, 1032, 1051, 1075, 1090, 1125 A2402: 133, 308, 502, 797, 939, 960			
CP0581	hypothetical protein	11-19,34-53,55-91,113-119,122-129,131-140,157-170,173-179,188-195,200-206,208-220,222-232,236-244,250-265,267-274,282-290,293-301,317-323,336-343,355-361,372-384	33-54, 69-95, 210-221, 244-254, 257-269	A0201: 32, 37, 43, 47, 50, 53, 57, 64, 68, 71, 73, 74, 78, 80, 82, 113, 120, 155, 162, 194, 205, 209, 231, 235, 238, 252, 259, 266, 273, 280, 287, 294, 301, 308, 315, 333 B0702: 8, 16, 18, 66, 377 A03: 36, 44, 81, 99, 124, 193, 261, 319 A2402: none	A:2	324-351	1
CP0618	leucyl-tRNA synthetase	31-55,58-64,69-75,81-90,129-150,154-167,179-184,189-208,227-237,248-	1-9, 31-46, 52-61, 60-78, 132-148, 182-199, 214-229, 249-264, 280-293, 320-341, 347-	A0201: 51, 82, 139, 186, 193, 197, 200, 239, 248, 249, 250, 257, 311, 325, 326, 520, 555, 556, 589, 606, 651, 716, 723,	A:7	90-100	

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		271,277-284,313-340,350-358,361-368,371-378,384-390,418-425,438-444,455-468,487-506,514-523,525-550,558-569,572-578,588-598,607-618,645-651,653-665,672-684,708-715,717-742,754-771,776-782,786-802,806-817	355, 386-411, 486-502, 553-575, 624-634, 673-689, 690-700, 702-714, 721-735, 736-746, 757-777, 788-798, 810-818	730, 737, 758, 761, 772, 788 **B0702:** 39, 41, 569, 695, 709, 783 **A03:** 51, 60, 89, 110, 141, 207, 216, 295, 301, 395, 404, 518, 527, 555, 568, 593, 596, 673, 691, 722, 757, 772, 790, 799 **A2402:**130, 131, 179, 402, 414, 701			
CP0693	DNA-directed RNA polymerase, beta` subunit	13-19,22-28,61-67,74-81,86-103,110-122,141-155,162-169,171-177,181-186,192-199,201-207,225-238,246-263,273-279,287-300,307-313,331-336,351-367,370-376,380-392,395-402,415-422,424-451,454-465,473-492,496-509,515-523,541-547,569-582,589-601,613-636,638-647,653-679,702-714,721-729,739-748,768-779,799-813,821-828,832-840,847-853,857-873,886-892,894-905,917-926,958-	25-43, 81-92, 111-141, 150-159, 213-220, 222-242, 243-254, 256-267, 276-288, 289-307, 381-397, 398-409, 422-438, 441-464, 485-500, 515-528, 542-553, 569-585, 591-601, 639-649, 656-664, 709-719, 725-734, 739-753, 841-850, 883-893, 902-911, 912-926, 935-948, 960-969, 976-984, 994-1008, 1037-1047,	**A0201:** 107, 110, 112, 133, 152, 200, 204, 223, 244, 251, 271, 289, 291, 305, 323, 360, 380, 407, 422, 428, 440, 491, 507, 512, 536, 616, 625, 628, 648, 650, 665, 668, 748, 768, 784, 797, 801, 826, 858, 859, 903, 910, 913, 925, 932, 959, 960, 968, 993, 1008, 1020, 1068, 1072, 1138, 1141, 1142, 1193, 1201, 1218, 1226, 1237, 1261, 1271, 1311, 1348, 1349, 1377 **B0702:** 126, 375, 433, 477, 608, 658, 852, 1106, 1121,	A : 3	273-290	19, 79

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	(
		971,974-981,983-989,997-1004,1006-1032,1034-1049,1054-1061,1063-1069,1073-1081,1083-1095,1097-1115,1122-1132,1143-1153,1164-1171,1178-1185,1193-1213,1216-1251,1258-1272,1277-1283,1305-1317,1324-1330,1333-1355,1383-1390	1073-1085, 1100-1108, 1124-1134, 1167-1179, 1194-1203, 1220-1254, 1258-1277, 1308-1319, 1348-1366	1303, 1362 **A03:** 24, 102, 151, 164, 169, 211, 229, 245, 274, 279, 285, 333, 348, 361, 382, 391, 397, 428, 447, 453, 480, 496, 590, 591, 595, 615, 623, 629, 638, 664, 669, 672, 738, 744, 775, 789, 840, 910, 917, 939, 966, 977, 1057, 1084, 1096, 1119, 1127, 1128, 1145, 1163, 1167, 1202, 1214, 1238, 1244, 1260, 1279, 1335 **A2402:** 145, 355, 961, 1053, 1103, 1245			
CP0737	phosphoenol pyruvate-protein phosphotransferase	16-23,25-47,49-59,64-72,79-91,95-105,113-122,133-145,148-162,169-176,179-188,190-200,202-218,232-239,250-283,299-333,337-344,349-355,364-406,430-437,439-449,452-460,464-490,492-503,505-530,533-562	12-21, 28-39, 52-67, 115-124, 189-204, 224-232, 234-242, 263-284, 302-322, 363-385, 389-397, 446-463, 479-488, 513-522, 528-552	**A0201:** 23, 30, 58, 78, 84, 97, 98, 120, 123, 133, 162, 169, 189, 215, 218, 236, 309, 312, 316, 365, 372, 384, 388, 391, 426, 446, 453, 465, 466, 478, 508, 513, 515, 523, 530, 536, 543, 554 **B0702:** 333, 467 **A03:** 13, 19, 115, 130, 181, 195, 225, 262, 270, 275, 311, 313, 325, 342, 390, 391, 398, 461, 530 **A2402:** 116, 188, 229	A:9	401-419	2
CP0840	fumarate hydratase	8-16,36-54,59-76,85-92,104-124,137-180,199-248,255-298,300-307,324-	18-27, 36-56, 101-120, 145-158, 165-173, 179-189, 239-	**A0201:** 5, 102, 149, 156, 160, 164, 185, 186, 204, 208, 211, 221, 232, 264, 270,	B:3	83-232	2

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		339,356-373,381-393,402-442,448-455	255, 255-270, 330-346, 355-375, 383-394, 403-421	273, 277, 280, 284, 287, 317, 329, 362, 387, 398, 402, 404, 422, 429, 431, 449 **B0702:** 37, 298, 359 **A03:** 9, 17, 35, 40, 41, 105, 111, 146, 166, 234, 279, 343, 384, 412 **A2402:** 365			
CP0888	conserved hypothetical protein	29-69,71-88,95-104,106-130,143-189,205-232	24-40, 46-64, 65-79, 83-105, 121-129, 144-199, 206-236	**A0201:** 30, 37, 66, 77, 81, 84, 112, 118, 141, 144, 145, 146, 149, 150, 153, 167, 169, 170, 178, 196, 213, 215, 220 **B0702:** none **A03:** 13, 21, 39, 44, 62, 75, 78, 97, 119, 124, 145, 148, 154, 177, 190, 207 **A2402:** 22, 216	A:3	182-199	22, 82
CP0897	polymorphic membrane protein, D family	4-46,51-66,77-88,102-110,115-126,142-148,171-181,183-192,202-212,227-234,251-261,263-278,283-316,319-325,336-352,362-371,386-393,399-406,410-425,427-437,441-450,457-464,471-476,490-496,514-521,549-557,571-578,601-611,618-623,627-646,657-670,672-689,696-704,726-740,742-756,765-776,778-784,792-801,822-836,862-868,875-881,887-	1-28, 109-124, 208-220, 261-280, 286-296, 310-324, 398-405, 425-433, 439-454, 504-517, 535-555, 570-591, 599-614, 620-630, 691-699, 711-719, 729-739, 751-760, 783-791, 843-855, 878-886, 890-900, 940-955, 984-1003, 1007-1026, 1065-1073, 1106-1122, 1136-1149, 1188-1198,	**A0201:** 26, 33, 79, 170, 200, 265, 290, 297, 302, 304, 333, 334, 377, 412, 414, 415, 431, 436, 458, 465, 481, 494, 536, 546, 568, 605, 678, 690, 697, 703, 724, 729, 730, 735, 737, 767, 776, 797, 840, 861, 938, 968, 999, 1072, 1079, 1085, 1094, 1113, 1160, 1163, 1180, 1188, 1195, 1217, 1245, 1250, 1273, 1302, 1358, 1362, 1363, 1401, 1408, 1465, 1469, 1481, 1507 **B0702:** 178, 960,	A:5	911-935	23, 83

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	S (I P
		898,914-919,941-948,963-969,971-978,996-1004,1007-1016,1036-1051,1068-1080,1082-1090,1092-1098,1104-1127,1135-1144,1156-1177,1181-1195,1197-1206,1214-1231,1243-1263,1278-1284,1295-1303,1305-1323,1337-1346,1355-1374,1376-1383,1406-1423,1455-1463,1465-1489,1506-1518,1527-1552,1555-1570,1581-1589	1203-1211, 1227-1235, 1249-1256, 1298-1308, 1374-1392, 1398-1409, 1414-1429, 1436-1444, 1456-1490, 1504-1521, 1530-1547, 1592-1609	1034 **A03:** 6, 21, 38, 159, 204, 248, 260, 306, 337, 349, 384, 425, 438, 458, 481, 502, 521, 546, 605, 690, 730, 731, 819, 860, 915, 946, 967, 1007, 1018, 1065, 1113, 1187, 1188, 1205, 1223, 1409, 1414, 1495, 1526, 1531, 1537 **A2402:** 101, 255, 1421, 1457, 1538, 1580, 1589			
CP0945	conserved hypothetical protein	15-25,41-102,111-117,127-134,145-170,194-201,207-225	10-30, 36-44, 46-59, 57-98, 122-138, 144-160, 162-173, 194-217	**A0201:** 12, 16, 37, 46, 61, 82, 121, 128, 149, 157, 162, 197, 204, 212 **B0702:** 39 **A03:** 2, 23, 53, 68, 97, 107, 121, 127, 156, 169, 196 **A2402:** 9, 13, 114	A:7	118-131	2
CP0973	transketolase	7-54,65-94,97-103,154-163,170-180,182-199,216-222,227-234,243-256,267-273,286-298,314-322,324-353,363-380,393-401,424-431,434-441,447-470,475-495,506-532,540-548,554-592,594-607,609-617,619-626,628-634,656-662	8-31, 43-59, 61-75, 93-104, 126-144, 179-201, 244-254, 289-302, 330-338, 364-382, 413-421, 428-466, 476-525, 582-599, 602-619, 621-632	**A0201:** 9, 10, 13, 35, 46, 76, 77, 83, 151, 165, 179, 187, 195, 283, 326, 338, 342, 360, 365, 368, 375, 415, 450, 485, 508, 556, 565, 569, 576, 602 **B0702:** none **A03:** 5, 20, 130, 181, 251, 271, 288, 294, 333, 355, 356, 364, 446, 451, 467, 483, 486, 523, 544, 611 **A2402:** 214, 219, 323, 399, 424, 458	A:2	115-128	2

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
CP0981	RNA methyltransferase, TrmA family	5-21,32-56,88-99,117-124,128-138,143-150,168-180,183-189,196-213,220-240,254-263,266-289,300-313,321-330,335-358,361-371,380-398	50-65, 67-87, 96-104, 144-153, 156-164, 169-177, 199-220, 259-289, 324-333, 339-360, 372-385	**A0201:** 26, 33, 49, 88, 96, 129, 169, 170, 198, 257, 268, 281, 337, 342, 366, 391, 393 **B0702:** 39, 122, 248 **A03:** 76, 106, 117, 185, 190, 198, 238, 257, 266, 280, 341, 344, 350, 367 **A2402:**304, 384	A:2	74-93	26, 86
CP1063	conserved hypothetical protein	12-23,44-50,54-60,91-97,103-109,119-125,131-137,141-151,172-183,201-226,230-238,252-265,315-321,331-345,360-370,376-386,392-406,410-416,422-431	133-159, 208-222, 354-368	**A0201:** 47, 134, 140, 143, 203, 204, 210, 254, 355, 358, 359, 362, 369, 417 **B0702:** 119 **A03:** 17, 128, 129, 141, 143, 153, 208, 232, 245, 278, 301, 313, 327, 328, 384, 395 **A2402:** none	B:4	1-88	27, 87
CP1075	hypothetical protein	4-16,29-36,39-64,69-75,79-87,90-122,126-134,139-173,184-190,195-203,206-213,216-228,234-246,250-257,260-266,274-282,291-312,318-325,340-345,348-361,364-388,399-437,439-448,451-464,467-473,480-510,514-520,534-553,561-574,579-589,593-599,616-655,658-671	3-12, 23-38, 27-38, 43-56, 93-107, 123-137, 144-154, 175-199, 229-244, 288-303,.308-316, 323-337, 410-423, 455-473, 488-496, 531-551, 560-577, 577-591, 619-637, 646-660, 664-672	**A0201:** 36, 101, 123, 129, 136, 146, 156, 160, 194, 205, 219, 236, 245, 283, 289, 350, 402, 413, 437, 475, 505, 517, 542, 585, 605, 620, 627, 657 **B0702:** 34, 52, 88, 358, 540, 656 **A03:** 3, 8, 13, 32, 82, 105, 111, 117, 137, 167, 173, 180, 182, 262, 300, 306, 350, 409, 412, 423, 499, 500, 563, 568, 581, 585, 627, 628 **A2402:** 554, 638	A:1	553-570	28, 88
CP1121	conserved	4-31,50-80,83-93,97-	1-17, 20-30, 66-	**A0201:** 4, 65, 66,	A:6	49-60, 582-	29, 89

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	S (I F
	hypothetical protein	103,111-116,123-132,134-163,170-199,205-210,215-220,230-247,249-278,280-308,311-329,337-347,349-358,365-371,376-401,417-430,434-446,459-505,511-518,527-535,537-545,547-565,573-581,592-601	80, 100-119, 139-150, 171-182, 186-198, 207-221, 228-242, 258-274, 286-308, 314-330, 337-352, 355-376, 383-391, 417-432, 437-446, 462-473, 479-488, 496-507, 514-522, 541-554, 557-565, 576-585, 589-605	120, 121, 144, 170, 174, 208, 226, 233, 276, 278, 285, 286, 298, 336, 348, 355, 363, 382, 384, 395, 457, 458, 494, 501, 578 **B0702:** 133, 278, 294, 551 **A03:** 53, 89, 110, 159, 186, 232, 290, 324, 406, 431, 458, 463, 480, 490, 513, 541, 549, 558, 585 **A2402:** 22, 137, 152, 189, 227, 255, 261, 291, 419, 569		607	
CP1126	conserved hypothetical protein	9-60,67-73,79-93,109-122,134-142,144-153,165-192,197-225,235-244,259-279,289-299,308-317,321-332,338-347,350-361,373-387,402-409,411-421,439-445,450-456,462-468,470-479,490-501,503-516	16-27, 49-60, 99-122, 136-145, 148-162, 186-194, 213-221, 225-246, 261-275, 281-292, 353-361, 390-401, 451-470, 486-494, 497-516	**A0201:** 15, 22, 28, 29, 48, 49, 106, 107, 114, 147, 170, 177, 188, 208, 209, 212, 256, 280, 287, 316, 451, 468, 489 **B0702:** 33, 217 **A03:** 36, 98, 124, 136, 142, 153, 177, 188, 251, 262, 291, 320, 323, 383, 417, 464, 487, 491, 492, 505 **A2402:** 44, 86, 146, 411, 437, 499	A:4	478-490	3
ARF0271	31aa (M at 2)	4-10,16-28	3-14, 16-30	**A0201:** none **B0702:** none **A03:** 1, 15 **A2402:** none	A:4, B:7	2-16	3
ARF0276	33aa (none)	8-18,20-30	none	**A0201:** none **B0702:** none **A03:** none **A2402:** none	A:2	7-15	3

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
ARF0280.1	30aa (none)	4-16,18-27	2-13, 20-30	A0201: 22 B0702: none A03: 1 A2402: none	A:1	10-29	33, 93
ARF0280.2	101aa (none)	36-57,62-92	46-66	A0201: 84 B0702: none A03: none A2402: none	A:3	27-35	34, 94
ARF0294	21aa (V at 4)	4-18	1-16	A0201: 1, 9 B0702: 2 A03: none A2402: none	A:8	5-12	35, 95
ARF0311	63aa (none)	13-27,38-52	1-13, 11-25, 27-37	A0201: 16, 37 B0702: none A03: 20 A2402: none	A:3	17-36	36, 96
ARF0524	69aa (M at 16)	4-17,27-40,55-62	9-25, 34-46, 50-64	A0201: 7, 10 B0702: none A03: 11, 14, 58 A2402: none	A:3	47-62	37, 97
ARF0636	12aa (none)	4-9	none	A0201: none B0702: none A03: none A2402: none	A:4	1-10	38, 98
ARF0857	25aa (none)	none	3-14	A0201: 2 B0702: none A03: 1 A2402: none	A:5	7-20	39, 99
ARF1016	32aa (none)	7-12,24-29	22-30	A0201: none B0702: none A03: 4, 9 A2402: none	A:3	7-21	40, 100
ARF1046	33aa (none)	14-30	15-30	A0201: none B0702: none A03: 1, 20 A2402: none	A:2	3-18	41, 101
ARF1062	20aa (none)	none	none	A0201: none B0702: none A03: 1 A2402: none	A:8, B:10	3-17	42, 102

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	(I I
ARF1071	113aa (M at 8)	4-27,31-59,75-86,93-103,105-110	15-44, 51-61, 79-95	A0201: 11, 15, 24, 28, 31, 35, 36, 42, 48, 49, 53, 78, 79, 97 B0702: none A03: 20, 28, 35, 37, 43, 49, 60, 65, 77, 85, 86 A2402: 21, 103	A:7	41-50	43
ARF1081	20aa (none)	4-13	none	A0201: none B0702: none A03: 7, 10 A2402: none	A:6	2-14	44
CRF0014	55a (M at 27)	4-15,17-23,39-52	4-13, 16-29, 40-50	A0201: 3, 38 B0702: none A03: 14, 41 A2402: none	A:4	33-41	4
CRF0016	26aa (none)	none	none	A0201: none B0702: none A03: none A2402: none	A:18	4-25	4
CRF0177	128aa (M at 31) no homology	8-19,40-47,67-86,88-125	15-25, 48-59, 64-80, 108-118	A0201: 7, 110 B0702: none A03: 16, 34, 109 A2402: none	A:5	60-70	4
CRF0434	49aa (V at 8)	4-27,41-46,	none	A0201: 19 B0702: none A03: 1, 23 A2402: none	A:3	30-47	4
CRF0435	48aa (V at 10)	21-28, 34-43	8-16	A0201: 34 B0702: none A03: 19, 28, 39 A2402: none	A:8	23-42	4
CRF0485	116aa (M at 5) No Homology	8-20,24-37,39-50,61-67,69-91	4-16, 31-42, 84-93	A0201: 4, 24, 79, 83 B0702: none A03: 7, 25, 71, 79, 91 A2402: none	A:7	42-59	5
CRF0507	148aa (M at 8), No homology	4-25,31-39,59-97,100-118,120-129	26-40, 49-57, 66-95, 97-128, 131-139	A0201: 8, 24, 61, 67, 72, 103, 112 B0702: none A03: 3, 39, 74, 110,	A:8	38-47	5

Chlamydia pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa*	Predicted class II-restricted T cell epitope/regions**	Predicted class I-restricted T cell epitope/regions***	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
				119 A2402: none			
CRF0551	60aa (V at 10)	7-24,32-43,45-57	32-48	A0201: 14, 18 B0702: none A03: 38, 47 A2402: 14	A:5	27-43	52, 112
CRF0586	63aa (M at 1)	4-18,20-26,31-37	3-17, 33-43	A0201: 3, 7, 10 B0702: none A03: 9 A2402: none	A:7	34-53	53, 113
CRF0686	85aa (M at 3)	15-23,25-39,43-50,62-70	16-32, 61-73	A0201: none B0702: 8 A03: 64 A2402: none	A:4	67-84	54, 114
CRF0754	45aa (none)	4-13,28-42	3-14, 28-39	A0201: 31 B0702: none A03: 7 A2402: 5	A:12	1-20	55,115
CRF0944	29aa (none)	4-10,19-26	21-29	A0201: none B0702: none A03: none A2402: none	A :12	5-13	56, 116
CRF0961	86aa (none)	4-22,40-46,51-57,64-76	2-10, 45-53, 58-72, 73-82	A0201: 35, 76 B0702: 3 A03: 1, 66 A2402: none	A:9, B:2	33-45	57, 117
CRF1037	45aa (none)	12-24,27-42	13-30, 34-44	A0201: 36 B0702: none A03: 15, 18 A2402: none	A:5	1-9	58, 118
CRF1073	69aa (none)	4-55	5-15, 17-33	A0201: 14 B0702: none A03: 53 A2402: none	A:8	26-45	59, 119
CRF1083	95aa (M at 8)	31-42,45-52,86-92	8-16, 35-52, 83-91	A0201: 86 B0702: 56 A03: 21 A2402: 4	B:26	27-93	60, 120

Table 2. Immunogenicity of peptide epitopes with human sera

Peptide	location in protein (aa)	Score	Seq. ID
CP0018.1	237 - 256	6	61
CP0018.2	508 - 530	1	61
CP0051.3	227 - 239	5	62
CP0069.1	141 - 160	1	63
CP0069.2	168 - 187	1	63
CP0069.3	155 - 173	3	63
CP0070.1	101 - 124	2	64
CP0070.2	161 - 187	1	64
CP0070.4	59 - 85	1	64
CP0070.5	80 - 106	1	64
CP0161.1	97 - 112	38	66
CP0177.3	139 - 165	1	67
CP0254.1	10 - 21	6	68
CP0282.1	667 - 688	15	69
CP0282.2	677 - 696	15	69
CP0282.3	161 - 187	24	69
CP0282.4	183 - 209	9	69
CP0282.5	205 - 231	6	69
CP0282.6	226 - 252	5	69
CP0286.1	603 - 629	7	70
CP0286.2	622 - 648	8	70
CP0286.3	643 - 669	4	70
CP0306.1	529 - 541	11	71
CP0316.1	12 - 34	12	72
CP0316.2	29 - 51	35	72
CP0316.3	46 - 67	5	72
CP0316.4	62 - 83	5	72
CP0339.1	139 - 151	4	73
CP0353.1	246 - 262	11	74
CP0353.2	251 - 275	16	74
CP0426.1	61 - 84	12	75
CP0426.2	79 - 102	23	75
CP0426.3	97 - 120	7	75
CP0426.4	115 - 138	5	75
CP0578.1	325 - 350	5	76
CP0578.2	345 - 370	6	76
CP0578.3	365 - 389	1	76
CP0581.1	324 - 349	11	77
CP0581.2	336 - 351	8	77
CP0618.1	90 - 100	2	78
CP0693.1	274 - 290	26	79
CP0737.1	401 - 419	25	80
CP0840.1	84 - 107	3	81
CP0840.2	101 - 123	3	81
CP0840.3	117 - 139	11	81
CP0888.1	182 - 199	9	82
CP0897.1	911 - 935	14	83

CP0945.1	118 - 131	11	84
CP0973.1	115 - 128	1	85
CP0981.1	74 - 93	5	86
CP1063.2	21 - 43	5	87
CP1063.4	54 - 76	2	87
CP1075.1	554 - 570	8	88
CP1126.2	478 - 490	4	90
ARF0271.1	2 - 14	4	91
ARF0276.1	7 - 15	3	92
ARF0280.1	10 - 28	4	93
ARF0280.2	27 - 34	1	94
ARF0311.1	17 - 35	6	96
ARF0524.1	47 - 61	6	97
ARF0636.1	1 - 10	1	98
ARF0857.1	7 - 20	9	99
ARF1016.1	7 - 20	2	100
ARF1046.1	3 - 17	7	101
ARF1062.1	3 - 17	59	102
ARF1071.1	41 - 50	1	103
ARF1081.1	2 - 14	1	104
CRF0014.1	33 - 41	1	105
CRF0016.1	4 - 25	77	106
CRF0177.1	60 - 69	2	107
CRF0435.1	23 - 41	13	109
CRF0485.1	42 - 59	4	110
CRF0507.1	38 - 46	1	111
CRF0551.1	27 - 43	13	112
CRF0586.1	34 - 53	6	113
CRF0686.1	67 - 84	2	114
CRF0754.1	1 - 20	4	115
CRF0961.1	33 - 45	6	117
CRF1073.1	26 - 45	25	119
CRF1083.1	27 - 53	8	120

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Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:
   a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 31-60.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.

3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from Seq ID No 5, 7-8, 14-16, 18-22, 24-27, 29-30.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

4. The nucleic acid molecule according to any one of the claims 1, 2, or 3, wherein the nucleic acid is DNA.

5. The nucleic acid molecule according to any one of the claims 1,2, 3, or 4, wherein the nucleic acid is RNA.

6. An isolated nucleic acid molecule according to any one of claims 1 to 4, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a C. *pneumoniae* genomic DNA.

7. A vector comprising a nucleic acid molecule according to any one of claims 1 to 6.

8. A vector according to claim 7, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 6.

9. A host cell comprising the vector according to claim 7 or 8.

10. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 4, 5 or 6 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 91-120.

11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a

nucleic acid molecule according to any one of the claims 3, 4, 5, or 6 and fragments there wherein the amino acid sequence is selected from the group consisting of Seq ID No 65, 67-68, 7 76, 78-82, 84-87, 89-90.

12. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptid comprising amino acid sequences of column "predicted immunogenic aa", "Predicted class II restricted T-Cell epitopes / regions" "Predicted class I restricted T-Cell epitope / regions", and "location of identified immunogenic region" of Table 1; the serum reactive peptide epitopes of Table 2, especially peptides comprising amino acids 18-29, 60-78, 89-95, 100-105, 124-143, 166-180, 187-194, 196-208, 224-242, 285-294, 305-311, 313-320, 351-360, 368-373, 390-403, 411-429, 432-470, 483-489, 513-523, 535-543, 548-564, 579-587, 589-598, 604-612, 622-627, 632-648, 55-84, 190-207, 323-331, 370-390, 551-570, 606-614, 633-647, 39-129, 224-296 and 464-609 of Seq ID No 61; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fro the position of: 60, 63, 67, 70, 126, 129, 133, 136, 169, 186, 200, 308, 371, 414, 421, 434, 444, 459, 503, 512, 532, 540, 547, 601, 625, 632, 634, 637, 99, 529, 25, 38, 59, 155, 278, 285, 412, 420, 441, 451, 457, 48 506, 510, 524, 536, 539, 554, 578, 596, 638, 179 and 604 of Seq ID No 61; 4-29, 31-38, 46-64, 66-80, 10 115, 131-139, 152-160, 170-183, 198-234, 239-255, 267-290, 301-313, 318-324, 336-345, 350-365, 380-38 65-82, 123-165, 268-290, 299-307, 320-329, 336-347, 76-103, 226-239 and 267-333 of Seq ID No 62; a fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fro the position of: 4, 13, 69, 93, 149, 174, 273, 277, 298, 305, 312, 319, 375, 28, 303, 3, 58, 73, 100, 153, 1 223, 227, 232, 251, 269, 286, 343, 374 and 238 of Seq ID No 62; 20-33, 35-43, 47-60, 77-92, 113-124, 137-145, 185-196, 66-75 and 92-214 of Seq ID No 63; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 32, 48, 49, 113, 77, 118, 139, 185, 2, 24 and 120 of Seq ID No 63; 47-64, 137-155, 157-167, 182-198, 212-233, 247-259, 29 303, 315-337, 345-350, 355-368, 373-379, 58-72, 183-196, 249-261, 315-323, 334-342, 347-356, 358-366 and 6-188 of Seq ID No 64; and fragments with at least 6 amino acid length, preferably at least amino acid length starting from the position of: 135, 160, 183, 184, 204, 249, 256, 293, 296, 318, 3 356, 372, 94, 13, 60, 159, 163, 189, 204, 220, 233, 300, 333, 335, 356, 362, 198 and 289 of Seq ID No 6 4-36, 43-49, 60-75, 96-107, 113-123, 132-172, 186-193, 217-229, 231-250, 260-282, 284-290, 298-312, 3 330, 5-38, 67-77, 113-127, 134-145, 147-156, 220-236, 271-283, 285-293, 296-304, 309-321 and 159-217 of Seq ID No 65; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 3, 10, 14, 17, 24, 46, 59, 133, 155, 220, 270, 312, 233, 2, 22 31, 36, 62, 65, 122, 140, 155, 162, 170, 189, 235, 248, 260, 286, 298, 156, 183 and 325 of Seq ID No 65 5-26, 29-50, 52-61, 65-74, 89-96, 140-147, 153-162, 183-188, 191-197, 203-210, 213-225, 1-9, 30-38, 53- 70-78, 92-107, 141-149, 158-166, 174-191, 205-224 and 97-113 of Seq ID No 66; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position 31, 33, 39, 56, 63, 78, 119, 136, 196, 14, 35, 38, 55, 97, 98, 146, 156, 158, 215, 88 and 214 of Seq ID N 66; 31-36, 46-54, 65-80, 86-102, 168-175, 179-186, 188-194, 200-208, 210-216, 225-231, 243-257, 289-2 362-387, 460-474, 476-486, 504-511, 518-525, 569-579, 581-600, 665-684, 688-694, 700-705, 717-735, 182-193, 202-211, 279-294, 311-319, 369-377, 468-476, 547-558, 579-587, 681-700, 731-740, 92-177 an 591-604 of Seq ID No 67; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 28, 78, 285, 309, 321, 376, 379, 388, 468, 475, 479, 500, 571, 624, 668, 716, 360, 455, 669, 185, 190, 204, 264, 281, 292, 478, 502, 588, 675, 680, 716 and 7 of Seq ID No 67; 4-9, 17-24, 27-52, 66-77, 91-98, 104-124, 127-139, 178-199, 211-219, 221-228, 234-2 246-255, 263-286, 303-312, 316-321, 337-346, 356-362, 367-372, 377-390, 402-416, 449-459, 465-479, 491-501, 503-508, 523-541, 551-558, 560-565, 31-69, 115-127, 132-143, 145-165, 176-187, 190-204, 21 220, 266-286, 304-316, 403-423, 440-456, 523-544 and 9-22 of Seq ID No 68; and fragments with a least 6 amino acid length, preferably at least 9 amino acid length starting from the position of 17, 24, 31, 45, 53, 56, 63, 69, 107, 129, 150, 171, 178, 189, 191, 217, 255, 273, 277, 305, 312, 451, 458, 4 478, 506, 522, 71, 379, 20, 29, 34, 44, 119, 133, 276, 284, 300, 328, 404, 465, 470, 529, 543, 182 and 55 Seq ID No 68; 34-42, 52-63, 71-87, 112-120, 142-147, 154-159, 166-177, 180-197, 204-224, 237-256, 2 268, 280-286, 312-324, 338-343, 372-412, 456-463, 479-490, 494-504, 506-512, 518-524, 538-548, 562-

585-591, 597-606, 674-690, 703-712, 714-740, 749-766, 95-103, 114-123, 180-195, 205-220, 240-248, 370-400, 481-495, 588-596, 707-715, 750-765, 160-253 and 630-717 of Seq ID No 69; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 179, 206, 209, 213, 216, 255, 286, 300, 304, 324, 365, 369, 373, 376, 377, 380, 381, 384, 562, 694, 720, 721, 729, 749, 752, 755, 197, 330, 559, 592, 600, 714, 751, 91, 111, 140, 167, 191, 315, 388, 393, 402, 458, 463, 587, 720, 762 and 748 of Seq ID No 69; 4-44, 50-55, 59-67, 73-83, 91-98, 101-109, 131-145, 230-236, 267-273, 293-300, 303-310, 349-354, 375-397, 404-416, 434-441, 445-452, 456-468, 479-485, 487-512, 544-568, 571-579, 593-599, 604-610, 614-621, 642-656, 665-678, 706-716, 729-736, 748-756, 780-795, 797-814, 827-844, 850-861, 864-882, 889-900, 906-933, 6-23, 28-36, 64-75, 134-150, 182-192, 227-236, 306-316, 340-350, 376-387, 421-435, 449-460, 527-535, 553-569, 587-595, 641-657, 668-676, 683-694, 743-755, 800-819, 843-865, 861-886, 894-915, 929-938 and 603-669 of Seq ID No 70; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 7, 8, 15, 73, 80, 133, 134, 138, 182, 194, 271, 272, 298, 432, 438, 457, 458, 487, 490, 527, 548, 568, 616, 644, 647, 667, 741, 782, 801, 829, 866, 126, 259, 792, 15, 20, 133, 155, 160, 232, 299, 458, 464, 552, 558, 560, 605, 607, 654, 670, 672, 768, 810, 840, 852, 877, 900, 167, 380, 425, 593 and 907 of Seq ID No 70; 4-32, 73-82, 90-101, 116-132, 144-160, 171-182, 195-200, 227-234, 255-271, 293-300, 313-336, 344-350, 369-375, 381-398, 413-421, 436-465, 487-496, 503-508, 510-527, 538-546, 552-562, 608-614, 617-636, 663-674, 679-691, 705-730, 734-748, 769-807, 825-834, 848-861, 864-871, 891-902, 7-16, 90-107, 110-137, 170-187, 197-213, 233-251, 277-287, 291-314, 361-390, 412-425, 451-465, 489-498, 513-521, 570-580, 619-637, 662-679, 713-721, 725-733, 745-754, 766-781, 790-805, 817-834, 868-883, 888-903 and 529-542 of Seq ID No 71; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8, 23, 53, 57, 128, 169, 178, 239, 263, 290, 297, 310, 324, 331, 339, 365, 398, 436, 443, 450, 470, 485, 488, 513, 514, 520, 614, 669, 711, 723, 771, 824, 849, 895, 316, 861, 118, 135, 196, 225, 284, 290, 370, 454, 489, 492, 521, 557, 624, 632, 745, 778, 783, 850, 868, 910, 226 and 383 of Seq ID No 71; 10-18, 30-52, 63-70, 72-79, 96-133, 146-158, 168-175, 184-193, 203-210, 213-222, 227-234, 237-257, 263-273, 285-291, 297-312, 320-338, 359-378, 385-393, 395-410, 412-421, 490-510, 521-527, 540-548, 563-571, 573-585, 592-598, 615-620, 632-641, 652-661, 672-679, 704-711, 717-723, 729-736, 742-751, 766-778, 788-808, 817-824, 836-842, 34-56, 73-89, 103-130, 146-154, 184-205, 213-227, 245-257, 258-278, 292-316, 331-341, 358-369, 372-383, 388-397, 410-418, 503-514, 524-530, 548-556, 565-573, 584-595, 637-646, 656-663, 673-686, 734-742, 745-754, 757-768, 770-781, 816-828 and 14-101 of Seq ID No 72; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 27, 32, 36, 65, 109, 112, 120, 127, 186, 249, 250, 262, 267, 297, 301, 353, 360, 367, 410, 418, 436, 465, 472, 505, 518, 522, 565, 576, 585, 638, 645, 650, 676, 687, 724, 745, 756, 763, 795, 164, 411, 510, 560, 569, 647, 766, 780, 14, 39, 48, 65, 74, 129, 175, 215, 217, 229, 230, 240, 253, 257, 262, 269, 308, 317, 322, 327, 352, 371, 372, 373, 374, 417, 443, 454, 472, 514, 525, 567, 629, 637, 657, 662, 683, 698, 731, 744, 752, 763, 769, 787, 790, 802, 815, 819, 26, 102, 381 and 704 of Seq ID No 72; 4-14, 20-33, 36-63, 71-93, 96-104, 106-117, 120-128, 131-147, 161-172, 174-186, 195-210, 212-247, 269-286, 288-301, 306-322, 324-332, 348-354, 356-363, 384-391, 35-66, 70-85, 107-118, 124-132, 165-179, 186-196, 197-205, 276-289, 292-300, 348-368, 369-381, 385-394 and 139-151 of Seq ID No 73; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 34, 41, 50, 53, 109, 127, 134, 153, 165, 271, 286, 297, 340, 384, 80, 321, 334, 354, 33, 57, 110, 153, 178, 276, 284, 383, 79, 99 and 123 of Seq ID No 73; 12-20, 37-48, 51-58, 69-75, 86-98, 113-136, 141-161, 171-216, 222-254, 264-273, 291-301, 311-345, 351-361, 31-39, 40-55, 62-74, 121-137, 148-164, 170-178, 223-253, 309-329, 354-369 and 246-275 of Seq ID No 74; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 46, 95, 103, 110, 143, 156, 178, 186, 190, 236, 242, 244, 291, 294, 315, 333, 353, 125, 183, 256, 326, 3, 68, 82, 102, 131, 177, 185, 190, 193, 223, 224, 244, 250, 295, 340, 349, 354, 88 and 89 of Seq ID No 74; 30-36, 50-56, 96-102, 110-116, 125-131, 162-174, 179-187, 189-201, 223-230, 232-239, 266-278, 320-328, 330-337, 339-350, 388-400, 408-413, 417-423, 435-447, 456-480, 499-524, 526-534, 53-62, 92-107, 192-203, 315-323, 436-452, 464-483, 502-524 and 61-138 of Seq ID No 75; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 126, 174, 225, 267, 309, 316, 320, 337, 436, 466, 467, 473, 474, 14, 128, 143, 228, 347, 494, 2, 52, 112, 201, 209, 217,

230, 235, 236, 337, 381, 395, 413, 419, 454, 466, 510, 515 and 556 of Seq ID No 75; 7-32, 36-56, 77-82, 88-100, 117-144, 153-166, 173-180, 188-226, 256-297, 300-316, 323-337, 339-348, 361-384, 390-427, 438 455, 476-488, 516-523, 535-566, 580-586, 597-607, 615-621, 626-634, 639-649, 654-660, 668-673, 677-68 707-714, 716-728, 730-742, 746-756, 763-772, 801-808, 820-829, 840-875, 882-888, 895-911, 914-920, 928-948, 953-961, 987-995, 999-1005, 1007-1026, 1053-1060, 1071-1079, 1082-1117, 1123-1129, 6-31, 37 48, 58-69, 90-105, 110-118, 134-142, 146-157, 210-220, 267-276, 291-300, 319-330, 362-372, 393-401, 405-421, 447-456, 463-471, 517-525, 574-582, 597-612, 618-626, 642-650, 656-668, 668-678, 683-695, 725-733, 778-791, 840-849, 894-917, 927-939, 954-963, 966-974, 978-998, 1010-1021, 1056-1067, 1070-1083, 1090-1104 and 325-389 of Seq ID No 76; **and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of:** 11, 18, 22, 41, 48, 86, 104, 15 190, 197, 221, 286, 290, 334, 343, 345, 407, 442, 509, 538, 575, 596, 597, 598, 636, 678, 685, 723, 754, 75 779, 818, 850, 857, 864, 893, 900, 901, 907, 918, 927, 934, 972, 988, 1018, 1025, 1034, 1048, 1065, 1072, 1089, 1094, 1101, 1108, 127, 336, 411, 806, 852, 28, 68, 90, 91, 93, 158, 293, 310, 350, 368, 380, 394, 425 441, 461, 554, 569, 597, 628, 667, 684, 724, 737, 752, 761, 767, 804, 851, 897, 907, 933, 979, 1030, 1032, 1051, 1075, 1090, 1125, 133, 308, 502, 797, 939 and 960 of Seq ID No 76; 11-19, 34-53, 55-91, 113-119 122-129, 131-140, 157-170, 173-179, 188-195, 200-206, 208-220, 222-232, 236-244, 250-265, 267-274, 282-290, 293-301, 317-323, 336-343, 355-361, 372-384, 33-54, 69-95, 210-221, 244-254, 257-269 and 32 351 of Seq ID No 77; **and fragments with at least 6 amino acid length, preferably at least 9 amir acid length starting from the position of:** 32, 37, 43, 47, 50, 53, 57, 64, 68, 71, 73, 74, 78, 80, 82, 113 120, 155, 162, 194, 205, 209, 231, 235, 238, 252, 259, 266, 273, 280, 287, 294, 301, 308, 315, 333, 8, 16, 1 66, 377, 36, 44, 81, 99, 124, 193, 261 and 319 of Seq ID No 77; 31-55, 58-64, 69-75, 81-90, 129-150, 15 167, 179-184, 189-208, 227-237, 248-271, 277-284, 313-340, 350-358, 361-368, 371-378, 384-390, 418-42 438-444, 455-468, 487-506, 514-523, 525-550, 558-569, 572-578, 588-598, 607-618, 645-651, 653-665, 672-684, 708-715, 717-742, 754-771, 776-782, 786-802, 806-817, 1-9, 31-46, 52-61, 60-78, 132-148, 182-199, 214-229, 249-264, 280-293, 320-341, 347-355, 386-411, 486-502, 553-575, 624-634, 673-689, 690-7 702-714, 721-735, 736-746, 757-777, 788-798, 810-818 and 90-100 of Seq ID No 78; **and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of:** 51, 82, 139, 186, 193, 197, 200, 239, 248, 249, 250, 257, 311, 325, 326, 520, 555, 556, 589, 606, 651, 716, 723, 730, 737, 758, 761, 772, 788, 39, 41, 569, 695, 709, 783, 51, 60, 89, 110, 141, 207, 21 295, 301, 395, 404, 518, 527, 555, 568, 593, 596, 673, 691, 722, 757, 772, 790, 799, 130, 131, 179, 402, 4 and 701 of Seq ID No 78;13-19, 22-28, 61-67, 74-81, 86-103, 110-122, 141-155, 162-169, 171-177, 181 186, 192-199, 201-207, 225-238, 246-263, 273-279, 287-300, 307-313, 331-336, 351-367, 370-376, 380-3 395-402, 415-422, 424-451, 454-465, 473-492, 496-509, 515-523, 541-547, 569-582, 589-601, 613-636, 638-647, 653-679, 702-714, 721-729, 739-748, 768-779, 799-813, 821-828, 832-840, 847-853, 857-873, 886-892, 894-905, 917-926, 958-971, 974-981, 983-989, 997-1004, 1006-1032, 1034-1049, 1054-1061, 1063-1069, 1073-1081, 1083-1095, 1097-1115, 1122-1132, 1143-1153, 1164-1171, 1178-1185, 1193-121 1216-1251, 1258-1272, 1277-1283, 1305-1317, 1324-1330, 1333-1355, 1383-1390, 25-43, 81-92, 111-141 150-159, 213-220, 222-242, 243-254, 256-267, 276-288, 289-307, 381-397, 398-409, 422-438, 441-464, 485-500, 515-528, 542-553, 569-585, 591-601, 639-649, 656-664, 709-719, 725-734, 739-753, 841-850, 883-893, 902-911, 912-926, 935-948, 960-969, 976-984, 994-1008, 1037-1047, 1073-1085, 1100-1108, 1124-1134, 1167-1179, 1194-1203, 1220-1254, 1258-1277, 1308-1319, 1348-1366 and 273-290 of Seq I No 79; **and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of:** 107, 110, 112, 133, 152, 200, 204, 223, 244, 251, 271, 289, 291, 305, 32 360, 380, 407, 422, 428, 440, 491, 507, 512, 536, 616, 625, 628, 648, 650, 665, 668, 748, 768, 784, 797, 8 826, 858, 859, 903, 910, 913, 925, 932, 959, 960, 968, 993, 1008, 1020, 1068, 1072, 1138, 1141, 1142, 11 1201, 1218, 1226, 1237, 1261, 1271, 1311, 1348, 1349, 1377, 126, 375, 433, 477, 608, 658, 852, 1106, 11 1303, 1362, 24, 102, 151, 164, 169, 211, 229, 245, 274, 279, 285, 333, 348, 361, 382, 391, 397, 428, 447, 453, 480, 496, 590, 591, 595, 615, 623, 629, 638, 664, 669, 672, 738, 744, 775, 789, 840, 910, 917, 939, 9 977, 1057, 1084, 1096, 1119, 1127, 1128, 1145, 1163, 1167, 1202, 1214, 1238, 1244, 1260, 1279, 1335, 1 355, 961, 1053, 1103 and 1245 of Seq ID No 79; 16-23, 25-47, 49-59, 64-72, 79-91, 95-105, 113-122, 1 145, 148-162, 169-176, 179-188, 190-200, 202-218, 232-239, 250-283, 299-333, 337-344, 349-355, 364-430-437, 439-449, 452-460, 464-490, 492-503, 505-530, 533-562, 12-21, 28-39, 52-67, 115-124, 189-20

224-232, 234-242, 263-284, 302-322, 363-385, 389-397, 446-463, 479-488, 513-522, 528-552 and 401-419 of Seq ID No 80; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 23, 30, 58, 78, 84, 97, 98, 120, 123, 133, 162, 169, 189, 215, 218, 236, 309, 312, 316, 365, 372, 384, 388, 391, 426, 446, 453, 465, 466, 478, 508, 513, 515, 523, 530, 536, 543, 554, 333, 467, 13, 19, 115, 130, 181, 195, 225, 262, 270, 275, 311, 313, 325, 342, 390, 391, 398, 461, 530, 116, 188 and 229 of Seq ID No 80;8-16, 36-54, 59-76, 85-92, 104-124, 137-180, 199-248, 255-298, 300-307, 324-339, 356-373, 381-393, 402-442, 448-455, 18-27, 36-56, 101-120, 145-158, 165-173, 179-189, 239-255, 255-270, 330-346, 355-375, 383-394, 403-421 and 83-232 of Seq ID No 81; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 5, 102, 149, 156, 160, 164, 185, 186, 204, 208, 211, 221, 232, 264, 270, 273, 277, 280, 284, 287, 317, 329, 362, 387, 398, 402, 404, 422, 429, 431, 449, 37, 298, 359, 9, 17, 35, 40, 41, 105, 111, 146, 166, 234, 279, 343, 384, 412 and 365 of Seq ID No 81; 29-69, 71-88, 95-104, 106-130, 143-189, 205-232, 24-40, 46-64, 65-79, 83-105, 121-129, 144-199, 206-236 and 182-199 of Seq ID No 82; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 30, 37, 66, 77, 81, 84, 112, 118, 141, 144, 145, 146, 149, 150, 153, 167, 169, 170, 178, 196, 213, 215, 220, 13, 21, 39, 44, 62, 75, 78, 97, 119, 124, 145, 148, 154, 177, 190, 207, 22 and 216 of Seq ID No 82; 4-46, 51-66, 77-88, 102-110, 115-126, 142-148, 171-181, 183-192, 202-212, 227-234, 251-261, 263-278, 283-316, 319-325, 336-352, 362-371, 386-393, 399-406, 410-425, 427-437, 441-450, 457-464, 471-476, 490-496, 514-521, 549-557, 571-578, 601-611, 618-623, 627-646, 657-670, 672-689, 696-704, 726-740, 742-756, 765-776, 778-784, 792-801, 822-836, 862-868, 875-881, 887-898, 914-919, 941-948, 963-969, 971-978, 996-1004, 1007-1016, 1036-1051, 1068-1080, 1082-1090, 1092-1098, 1104-1127, 1135-1144, 1156-1177, 1181-1195, 1197-1206, 1214-1231, 1243-1263, 1278-1284, 1295-1303, 1305-1323, 1337-1346, 1355-1374, 1376-1383, 1406-1423, 1455-1463, 1465-1489, 1506-1518, 1527-1552, 1555-1570, 1581-1589, 1-28, 109-124, 208-220, 261-280, 286-296, 310-324, 398-405, 425-433, 439-454, 504-517, 535-555, 570-591, 599-614, 620-630, 691-699, 711-719, 729-739, 751-760, 783-791, 843-855, 878-886, 890-900, 940-955, 984-1003, 1007-1026, 1065-1073, 1106-1122, 1136-1149, 1188-1198, 1203-1211, 1227-1235, 1249-1256, 1298-1308, 1374-1392, 1398-1409, 1414-1429, 1436-1444, 1456-1490, 1504-1521, 1530-1547, 1592-1609 and 911-935 of Seq ID No 83; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 26, 33, 79, 170, 200, 265, 290, 297, 302, 304, 333, 334, 377, 412, 414, 415, 431, 436, 458, 465, 481, 494, 536, 546, 568, 605, 678, 690, 697, 703, 724, 729, 730, 735, 737, 767, 776, 797, 840, 861, 938, 968, 999, 1072, 1079, 1085, 1094, 1113, 1160, 1163, 1180, 1188, 1195, 1217, 1245, 1250, 1273, 1302, 1358, 1362, 1363, 1401, 1408, 1465, 1469, 1481, 1507, 178, 960, 1034, 6, 21, 38, 159, 204, 248, 260, 306, 337, 349, 384, 425, 438, 458, 481, 502, 521, 546, 605, 690, 730, 731, 819, 860, 915, 946, 967, 1007, 1018, 1065, 1113, 1187, 1188, 1205, 1223, 1409, 1414, 1495, 1526, 1531, 1537, 101, 255, 1421, 1457, 1538, 1580 and 1589, of Seq ID No 83;15-25, 41-102, 111-117, 127-134, 145-170, 194-201, 207-225, 10-30, 36-44, 46-59, 57-98, 122-138, 144-160, 162-173, 194-217 and 118-131 of Seq ID No 84; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 12, 16, 37, 46, 61, 82, 121, 128, 149, 157, 162, 197, 204, 212, 39, 2, 23, 53, 68, 97, 107, 121, 127, 156, 169, 196, 9, 13 and 114 of Seq ID No 84; 7-54, 65-94, 97-103, 154-163, 170-180, 182-199, 216-222, 227-234, 243-256, 267-273, 286-298, 314-322, 324-353, 363-380, 393-401, 424-431, 434-441, 447-470, 475-495, 506-532, 540-548, 554-592, 594-607, 609-617, 619-626, 628-634, 656-662, 8-31, 43-59, 61-75, 93-104, 126-144, 179-201, 244-254, 289-302, 330-338, 364-382, 413-421, 428-466, 476-525, 582-599, 602-619 621-632 and 115-128 of Seq ID No 85; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 9, 10, 13, 35, 46, 76, 77, 83, 151, 165, 179, 187, 195, 283, 326, 338, 342, 360, 365, 368, 375, 415, 450, 485, 508, 556, 565, 569, 576, 602, 5, 20, 130, 181, 251, 271, 288, 294, 333, 355, 356, 364, 446, 451, 467, 483, 486, 523, 544, 611, 214, 219, 323, 399, 424 and 458, of Seq ID No 85; 5-21, 32-56, 88-99, 117-124, 128-138, 143-150, 168-180, 183-189, 196-213, 220-240, 254-263, 266-289, 300-313, 321-330, 335-358, 361-371, 380-398, 50-65, 67-87, 96-104, 144-153, 156-164, 169-177, 199-220, 259-289, 324-333, 339-360, 372-385 and 74-93 of Seq ID No 86; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 26, 33, 49, 88, 96, 129, 169, 170, 198, 257, 268, 281, 337, 342, 366, 391, 393, 39, 122, 248, 76, 106, 117, 185, 190, 198, 238, 257, 266, 280, 341, 344, 350, 367, 304 and 384 of

Seq ID No 86; 12-23, 44-50, 54-60, 91-97, 103-109, 119-125, 131-137, 141-151, 172-183, 201-226, 230-238, 252-265, 315-321, 331-345, 360-370, 376-386, 392-406, 410-416, 422-431, 133-159, 208-222, 354-36 and 1-88 of Seq ID No 87; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 47, 134, 140, 143, 203, 204, 210, 254, 355, 358, 359, 362, 369, 417, 119, 17, 128, 129, 141, 143, 153, 208, 232, 245, 278, 301, 313, 327, 328, 384 and 395 of Se ID No 87; 4-16, 29-36, 39-64, 69-75, 79-87, 90-122, 126-134, 139-173, 184-190, 195-203, 206-213, 216-228, 234-246, 250-257, 260-266, 274-282, 291-312, 318-325, 340-345, 348-361, 364-388, 399-437, 439-44 451-464, 467-473, 480-510, 514-520, 534-553, 561-574, 579-589, 593-599, 616-655, 658-671, 3-12, 23-38 27-38, 43-56, 93-107, 123-137, 144-154, 175-199, 229-244, 288-303, 308-316, 323-337, 410-423, 455-473 488-496, 531-551, 560-577, 577-591, 619-637, 646-660, 664-672 and 553-570 of Seq ID No 88; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fro the position of: 36, 101, 123, 129, 136, 146, 156, 160, 194, 205, 219, 236, 245, 283, 289, 350, 402, 413, 437, 475, 505, 517, 542, 585, 605, 620, 627, 657, 34, 52, 88, 358, 540, 656, 3, 8, 13, 32, 82, 105, 111, 117, 137, 167, 173, 180, 182, 262, 300, 306, 350, 409, 412, 423, 499, 500, 563, 568, 581, 585, 627, 628, 554 an 638 of Seq ID No 88; 4-31, 50-80, 83-93, 97-103, 111-116, 123-132, 134-163, 170-199, 205-210, 215-22 230-247, 249-278, 280-308, 311-329, 337-347, 349-358, 365-371, 376-401, 417-430, 434-446, 459-505, 511-518, 527-535, 537-545, 547-565, 573-581, 592-601, 1-17, 20-30, 66-80, 100-119, 139-150, 171-182, 186-198, 207-221, 228-242, 258-274, 286-308, 314-330, 337-352, 355-376, 383-391, 417-432, 437-446, 462-473, 479-488, 496-507, 514-522, 541-554, 557-565, 576-585, 589-605, 49-60 and 582-607 of Seq ID No 89; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 4, 65, 66, 120, 121, 144, 170, 174, 208, 226, 233, 276, 278, 285, 286, 29 336, 348, 355, 363, 382, 384, 395, 457, 458, 494, 501, 578, 133, 278, 294, 551, 53, 89, 110, 159, 186, 232, 290, 324, 406, 431, 458, 463, 480, 490, 513, 541, 549, 558, 585, 22, 137, 152, 189, 227, 255, 261, 291, 41 and 569 of Seq ID No 89; 9-60, 67-73, 79-93, 109-122, 134-142, 144-153, 165-192, 197-225, 235-244, 259-279, 289-299, 308-317, 321-332, 338-347, 350-361, 373-387, 402-409, 411-421, 439-445, 450-456, 462-468, 470-479, 490-501, 503-516, 16-27, 49-60, 99-122, 136-145, 148-162, 186-194, 213-221, 225-24 261-275, 281-292, 353-361, 390-401, 451-470, 486-494, 497-516 and 478-490 of Seq ID No 90; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting fr the position of: 15, 22, 28, 29, 48, 49, 106, 107, 114, 147, 170, 177, 188, 208, 209, 212, 256, 280, 287, 3 451, 468, 489, 33, 217, A03: 36, 98, 124, 136, 142, 153, 177, 188, 251, 262, 291, 320, 323, 383, 417, 464, 487, 491, 492, 505, 44, 86, 146, 411, 437 and 499 of Seq ID No 90; 4-10, 16-28, 3-14, 16-30 and 2-16 c Seq ID No 91; and fragments with at least 6 amino acid length, preferably at least 9 amino aci length starting from the position of: 1 and15 of Seq ID No 91; 8-18, 20-30 and 7-15 of Seq ID N 92; 4-16, 18-27, 2-13, 20-30 and 10-29 of Seq ID No 93; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 22 and 1 of Seq II No 93; 36-57, 62-92, 46-66 and 27-35 of Seq ID No 94; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 84 of Seq ID No 9 4-18, 1-16 and 5-12 of Seq ID No 95; and fragments with at least 6 amino acid length, preferab at least 9 amino acid length starting from the position of: 1, 9 and 2 of Seq ID No 95; 13-27, 38- 1-13, 11-25, 27-37 and 17-36 of Seq ID No 96; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 16, 37 and 20 of Seq ID N 96; 4-17, 27-40, 55-62, 9-25, 34-46, 50-64 and 47-62 of Seq ID No 97; and fragments with at least amino acid length, preferably at least 9 amino acid length starting from the position of: 7, 10, 14 and 58 of Seq ID No 97; 4-9, 1-10 of Seq ID No 98; 3-14 and 7-20 of Seq ID No 99; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting f the position of: 2 and 1 of Seq ID No 99; 7-12, 24-29, 22-30 and 7-21 of Seq ID No 100; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting f the position of: 4 and 9 of Seq ID No 100; 14-30, 15-30 and 3-18 of Seq ID No 101; and fragmen with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 1 and 20 of Seq ID No 101; 3-17 of Seq ID No 102; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 1 of S ID No 102; 4-27, 31-59, 75-86, 93-103, 105-110, 15-44, 51-61, 79-95 and 41-50 of Seq ID No 103; ar

fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 11, 15, 24, 28, 31, 35, 36, 42, 48, 49, 53, 78, 79, 97, 20, 28, 35, 37, 43, 49, 60, 65, 77, 85, 86, 21 and 103 of Seq ID No 103; 4-13 and 2-14 of Seq ID No 104; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 7 and 10 of Seq ID No 104; 4-15, 17-23, 39-52, 4-13, 16-29, 40-50 and 33-41 of Seq ID No 105; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 3, 38, 14 and 41 of Seq ID No 105; 4-25 of Seq ID No 106; 8-19, 40-47, 67-86, 88-125, 15-25, 48-59, 64-80, 108-118 and 60-70 of Seq ID No 107; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 7, 110, 16, 34 and 109 of Seq ID No 107; 4-27, 41-46, and 30-47 of Seq ID No 108; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 19, 1 and 23 of Seq ID No 108; 21-28, 34-43, 8-16 and 23-42 of Seq ID No 109; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 34, 19, 28 and 39 of Seq ID No 109; 8-20, 24-37, 39-50, 61-67, 69-91, 4-16, 31-42, 84-93 and 42-59 of Seq ID No 110; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 4, 24, 79, 83, 7, 25, 71, 79 and 91 of Seq ID No 110; 4-25, 31-39, 59-97, 100-118, 120-129, 26-40, 49-57, 66-95, 97-128, 131-139, 38-47 of Seq ID No 111; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8, 24, 61, 67, 72, 103, 112, 3, 39, 74, 110 and 119 of Seq ID No 111; 7-24, 32-43, 45-57, 32-48 and 27-43 of Seq ID No 112; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 14, 18, 38, 47 and 14 of Seq ID No 112; 4-18, 20-26, 31-37, 3-17, 33-43 and 34-53 of Seq ID No 113; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 3, 7, 10 and 9 of Seq ID No 113; 15-23, 25-39, 43-50, 62-70, 16-32, 61-73 and 67-84 of Seq ID No 114; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 8 and 64 of Seq ID No 114; 4-13, 28-42, 3-14, 28-39 and 1-20 of Seq ID No115; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 31, 7 and 5 of Seq ID No115; 4-10, 19-26, 21-29 and 5-13 of Seq ID No 116; 4-22, 40-46, 51-57, 64-76, 2-10, 45-53, 58-72, 73-82 and 33-45 of Seq ID No117; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 35, 76, 3, 1 and 66 of Seq ID No117; 12-24, 27-42, 13-30, 34-44 and 1-9 of Seq ID No 118; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 36, 15 and 18 of Seq ID No 118; 4-55, 5-15, 17-33 and 26-45 of Seq ID No 119; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 14 and 53 of Seq ID No 119; 31-42, 45-52, 86-92, 8-16, 35-52, 83-91 and 27-93 of Seq ID No 120; and fragments with at least 6 amino acid length, preferably at least 9 amino acid length starting from the position of: 86, 56, 21 and 4 of Seq ID No 120; 237 – 256, 508 – 530 of Seq ID No 61; 227 – 239 of Seq ID No 62; 141 – 160, 168 – 187, 155 – 173 of Seq ID No 63; 101 – 124, 161 – 187, 59 – 85, 80 – 106 of Seq ID No 64; 97 – 112 of Seq ID No 66; 139 – 165 of Seq ID No 67; 10 – 21 of Seq ID No 68; 667 – 688, 677 – 696, 161 – 187, 183 – 209, 205 – 231, 226 – 252 of Seq ID No 69; 603 – 629, 622 – 648, 643 – 669 of Seq ID No 70; 529 – 541 of Seq ID No 71; 12 – 34, 29 – 51, 46 – 67, 62 – 83 of Seq ID No 72; 139 – 151 of Seq ID No 73; 246 – 262, 251 – 275 of Seq ID No 74; 61 – 84, 79 – 102, 97 – 120, 115 – 138 of Seq ID No 75; 325 – 350, 345 – 370, 365 – 389 of Seq ID No 76; 324 – 349, 336 – 351 of Seq ID No 77; 90 – 100 of Seq ID No 78; 274 – 290 of Seq ID No 79; 401 – 419 of Seq ID No 80; 84 – 107, 101 – 123, 117 – 139 of Seq ID No 81; 182 – 199 of Seq ID No 82; 911 – 935 of Seq ID No 83; 118 – 131 of Seq ID No 84; 115 – 128 of Seq ID No 85; 74 – 93 of Seq ID No 86; 21 – 43, 54 – 76 of Seq ID No 87; 554 – 570 of Seq ID No 88; 478 – 490 of Seq ID No 90; 2 – 14 of Seq ID No 91; 7 – 15 of Seq ID No 92; 10 – 28 of Seq ID No 93; 27 – 34 of Seq ID No 94; 17 – 35 of Seq ID No 96; 47 – 61 of Seq ID No 97; 1-10 of Seq ID No 98; 7-20 of Seq ID No 99; 7-20 of Seq ID No 100; 3-17 of Seq ID No 101; 3-17 of Seq ID No 102; 41-50 of Seq ID No 103; 2-14 of Seq ID No 104; 33-41 of Seq ID No 105; 4-25 of Seq ID No 106; 60-69 of Seq ID No 107; 23-41 of Seq ID No 109; 42-59 of Seq ID No 110; 38-46 of Seq ID No 111; 27-43 of Seq ID No 112; 34-53 of Seq ID No 113; 67-84 of Seq ID No 114; 1-20 of

Seq ID No 115; 33-45 of Seq ID No 117; 26-45 of Seq ID No 119; 27-53 of Seq ID No 120, and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences.

13. A process for producing a *C. pneumoniae* hyperimmune serum reactive antigen or a fragme thereof according to any one of the claims 10 to 12 comprising expressing the nucleic acid molec according to any one of claims 1 to 6.

14. A process for producing a cell, which expresses a *C. pneumoniae* hyperimmune serum reacti antigen or a fragment thereof according to any one of the claims 10 to 12 comprising transformi or transfecting a suitable host cell with the vector according to claim 7 or claim 8.

15. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reacti antigen or a fragment thereof, as defined in any one of claims 10 to 12 or a nucleic acid molec according to any one of claims 1 to 6.

16. A pharmaceutical composition, especially a vaccine, according to claim 15, characterized in tha further comprises an immunostimulatory substance, preferably selected from the gro comprising polycationic polymers, especially polycationic peptides, immunostimulat deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroacti compounds, especially human growth hormone, alumn, Freund's complete or incompl adjuvants or combinations thereof.

17. Use of a nucleic acid molecule according to any one of claims 1 to 6 or a hyperimmune seru reactive antigen or fragment thereof according to any one of claims 10 to 12 for the manufacture a pharmaceutical preparation, especially for the manufacture of a vaccine against *C. pneumon* infection.

18. An antibody, or at least an effective part thereof, which binds at least to a selective part of hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 10 12.

19. An antibody according to claim 18, wherein the antibody is a monoclonal antibody.

20. An antibody according to claim 18 or 19, wherein said effective part comprises Fab fragments.

21. An antibody according to any one of claims 18 to 20, wherein the antibody is a chimeric antibody

22. An antibody according to any one of claims 18 to 21, wherein the antibody is a humani antibody.

23. A hybridoma cell line, which produces an antibody according to any one of claims 18 to 22.

24. A method for producing an antibody according to claim 18, characterized by the following steps
    - initiating an immune response in a non-human animal by administrating an hyperimm serum-reactive antigen or a fragment thereof, as defined in any one of the claims 10 to 12, said animal,
    - removing an antibody containing body fluid from said animal, and
    - producing the antibody by subjecting said antibody containing body fluid to furt purification steps.

25. Method for producing an antibody according to claim 19, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 10 to 12, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

26. Use of the antibodies according to any one of claims 18 to 22 for the preparation of a medicament for treating or preventing *C. pneumoniae* infections.

27. An antagonist, which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 10 to 12.

28. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 10 to 12 comprising:
   a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 10 to 12 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
   b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

29. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 10 to 12 to its interaction partner comprising:
   a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 10-12,
   b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 18 to 22,
   c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
   d) providing a candidate antagonist,
   e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
   f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

30. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 10 to 12 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

31. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 10 to 12 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 6 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 10-12.

32. A process for *in vitro* diagnosis of a bacterial infection, especially a *C. pneumoniae* infectic comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmu serum reactive antigen and fragment according to any one of claims 1 to 6 or the presence of t hyperimmune serum reactive antigen or fragment thereof according to any one of claims 10 to 12

33. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one claims 10 to 12 for the generation of a peptide binding to said hyperimmune serum reacti antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalin

34. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one claims 10 to 12 for the manufacture of a functional nucleic acid, wherein the functional nucleic ac is selected from the group comprising aptamers and spiegelmers.

35. Use of a nucleic acid molecule according to any one of claims 10 to 12 for the manufacture o functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the gro comprising ribozymes, antisense nucleic acids and siRNA.

Summary:

Chlamydia pneumoniae antigens

The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *C. pneumoniae*, methods for isolating such antigens and specific uses thereof.

[no Fig. on front page]

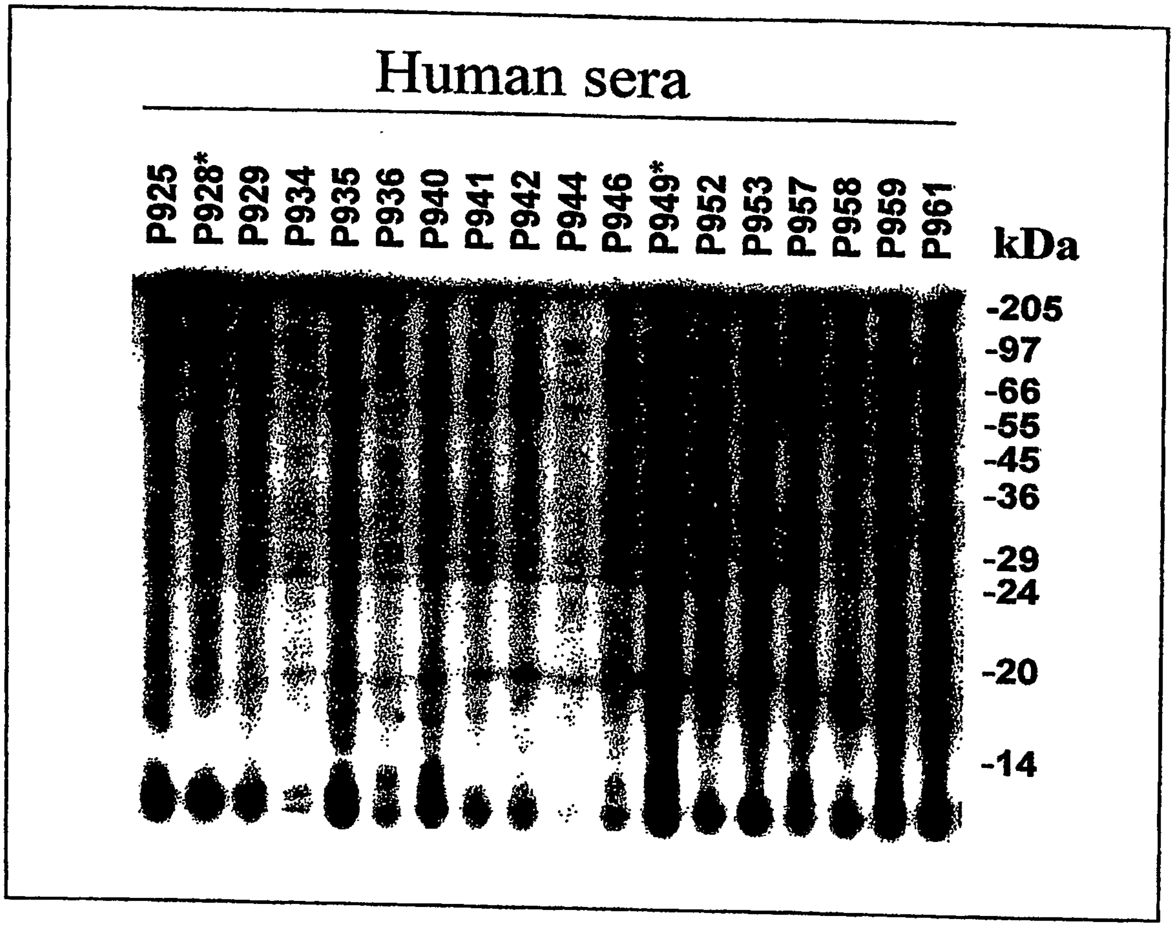
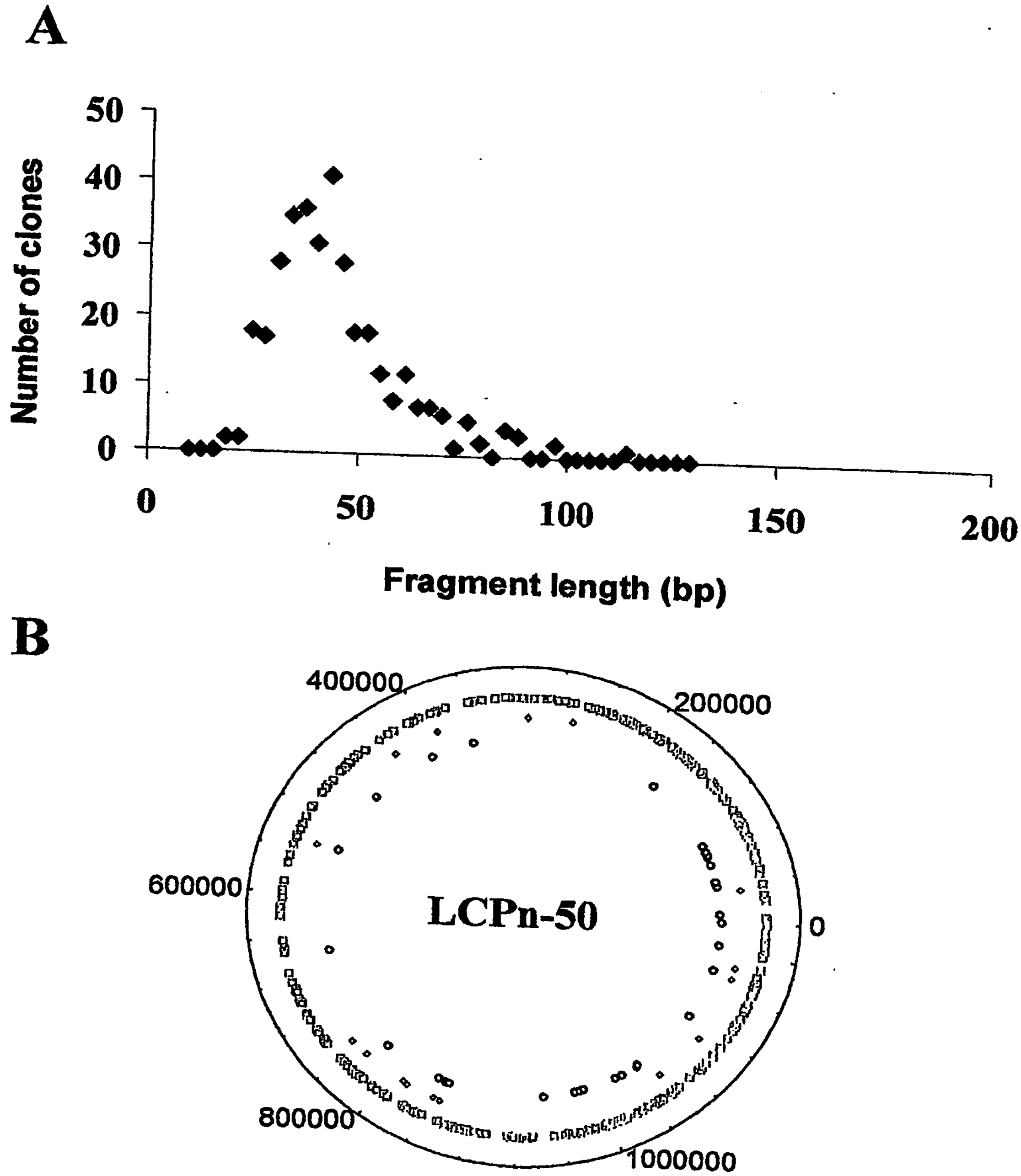

Human sera
P925
P928*
P929
P934
P935
P936
P940
P941
P942
P944
P946
P949*
P952
P953
P957
P958
P959
P961
kDa
-205
-97
-66
-55
-45
-36
-29
-24
-20
-14

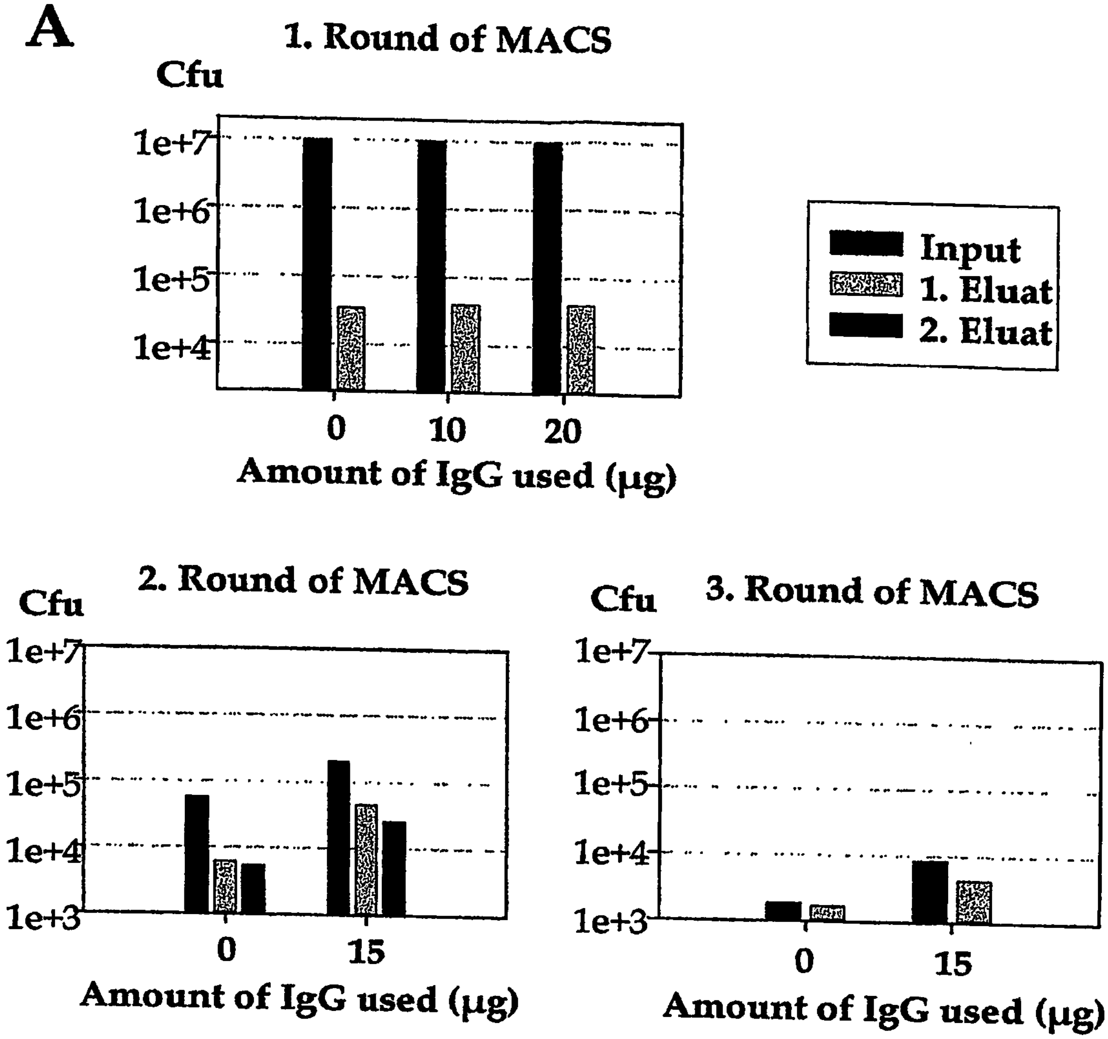
Fig. 1



	Total (trimmed)	390 (100.0 %)
□	**ORF** (+/+, +/-)	298 (76.4 %)
◇	**non-ORF** (+/+, +/-)	19 (4.9 %)
○	**chimeric**	31 (7.9 %)
	non-blastable	42 (10.8 %)

Fig. 2

A


1. Round of MACS
Cfu
1e+7
1e+6
1e+5
1e+4
0
10
20
Amount of IgG used (µg)
Input
1. Eluat
2. Eluat
2. Round of MACS
Cfu
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1e+5
1e+4
1e+3
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Amount of IgG used (µg)
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Amount of IgG used (µg)

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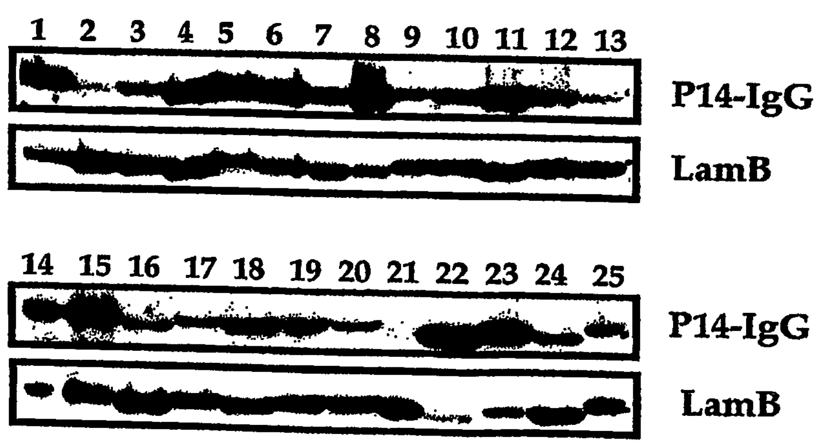
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Fig. 3

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<211> 2787

<212> DNA

<213> Chlamydia pneumoniae

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<211> 1215

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<213> Chlamydia pneumoniae

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<211> 3429

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<213> Chlamydia pneumoniae

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<211> 1383

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<211> 762

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<213> Chlamydia pneumoniae

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<210> 25

<211> 1998

<212> DNA

<213> Chlamydia pneumoniae

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<211> 1206

<212> DNA

<213> Chlamydia pneumoniae

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<210> 27
<211> 1335
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<211> 2025
<212> DNA
<213> Chlamydia pneumoniae

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<210> 29

<211> 1830

<212> DNA

<213> Chlamydia pneumoniae

<400> 29

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tcacccaata atagtatcaa cgactataag acgcagaagg cattagcatt ttgccaaaaa 1800
catcaatcta aggaccgagc tgcctcttag 1830

<210> 30

<211> 1596

<212> DNA

<213> Chlamydia pneumoniae

<400> 30
atgttgggca aagaagaaga gtttacgtgt aaacaaaagc agtgtttgtc acattttgtt 60
accaatctga cgtccgatgt atttgcttta aaaaatcttc cagaagtcgt taagggagct 120
ttattttcta aatactcccg ttcagtttta ggtttgcgag cacttttgtt aaaagaattt 180
ctatctaatg aagaggatgg agatgtttgt gacgaagcct atgacttcga aaccgatgta 240
cagaaagctg cggactttta ccaaagggtt cttgataatt ttggggatga ttctgtagga 300
gagcttggcg gagcccacct ggctatggaa aatgtctcta ttttggctgc taaagtttta 360
gaggatgctc gaattggcgg atccccgcta gaaaagtcca caagatacgt ctatttcgat 420
caaaaggtac ggggggagta tttatattac cgagacccta ttttgatgac ttcggccttt 480
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caaggtcatc aaaattaccg cactatagct acaggtttag tgcgagaggt tgtcaagttc 1500
aatcctatgt acgaattatt tttcaaattt gtagattatt ctgacataga tttaggacgg 1560
ttaaatcagg aaatgcgaaa agaaccaacg acctaa 1596

<210> 31

<211> 93

<212> DNA

<213> Chlamydia pneumoniae

<400> 31
cgcgtgatga aggcagtggt ctctcacaag agcaggacct cctctataca caggcagtac 60
agctcttatt ctttatttta cagcatcctc aag 93

<210> 32

<211> 99

<212> DNA

<213> Chlamydia pneumoniae

<400> 32
gacggagtta attttggaaa tcttttccag ccgtgccctt actgcagagg caaatatcca 60
agtccaactt gcacaagcac gttatctcct tcctcgtct 99

<210> 33

<211> 90

<212> DNA

<213> Chlamydia pneumoniae

<400> 33
ggcttacgac ggttttgcaa acgatactcc atagtagtat cggaaagtgg agagcctttc 60
tgcttactca agaaaaaaaa gatcttttg 90

<210> 34
<211> 303
<212> DNA
<213> Chlamydia pneumoniae

<400> 34
aacttcccaa tctgtgatag aagttccaga ttcagagggg attgcagaga cgaggatctc 60
tgcggaagaa atcgatacga ggctttccct gacgacaaga cagaaggtca tctttgctct 120
tgcgacactc ttgctcttag caagtattgc tgccttcata gtcacgggat ttggtggatt 180
gacagtcatg caagttctcc ttgttgcttc tgtaggatcg gcggttgctt ctgtaacact 240
ccctatggtt tcctcaggat tttcctacgt cgcctaccaa ctgaaagcaa gattgaatat 300
cag 303

<210> 35
<211> 63
<212> DNA
<213> Chlamydia pneumoniae

<400> 35
tttcttcctg tgttgccggg attattacta ggtcctcctt tacctcagat gtcgttcaga 60
ttg 63

<210> 36
<211> 189
<212> DNA
<213> Chlamydia pneumoniae

<400> 36
tttttcataa aatattctct ttcaaacgga tatgggattc aaaaatatct gcaaacaagg 60
ctctcagcta tacctgaatg gcatttttcc ggaacgaata ctagctcgaa aattaaaaaa 120
ctgtgcgaag agctatccca gaactgctct taccatagaa gtactggtat cctcggtctt 180
aggagctct 189

<210> 37

<211> 207

<212> DNA

<213> Chlamydia pneumoniae

<400> 37
tgcagctact ctgtttactc actatggagc ctcctacaac ttttgatgct gatgaaatca 60

gaaaagaaaa aatcaaaatt cttcaacgta tctcaccatt ttcagaaggt tcttcgattg 120

tccgaggaca atatggtcca ggaacggttc aaggagtctc ggtccttggc tatcgtgaag 180

aagagaatgt tgacaaagat tcccgag 207

<210> 38

<211> 36

<212> DNA

<213> Chlamydia pneumoniae

<400> 38
gcacaagcgt tcgggagcct actcctcagg atgcta 36

<210> 39

<211> 75

<212> DNA

<213> Chlamydia pneumoniae

<400> 39
gagctactca tttcctacca gagaaaaaca agctcagcta ttggaaaaaa gaactttacg 60

accagctcgc agtgt 75

<210> 40

<211> 96

<212> DNA

<213> Chlamydia pneumoniae

<400> 40
gaaggaagag aagatcttcc atcagcactt aggaaaggca gccccacaag cggcaacagc 60

aacttcagga gtgcagccta ctgcggatcc tgttgc 96

<210> 41

<211> 99

<212> DNA

<213> Chlamydia pneumoniae

<400> 41
cgccttagga gtacaacaaa cacctcccag tcaagtcctc aatgggattg cactcatcct 60

atctatttat gtgatgttcc ccacgggagt ggctatgta 99

<210> 42

<211> 60

<212> DNA

<213> Chlamydia pneumoniae

<400> 42
gctccccaag cccggggtga caccaagatc agaggttatc gaaatcggac tcgcgcttgc 60

<210> 43

<211> 339

<212> DNA

<213> Chlamydia pneumoniae

<400> 43
ggacgcttac tgaaacagtg tatgctatca agcttgcgca aatggctggc tatactacaa 60

ttatttctca tcgctcagga gaaactacgg acactacgat tgcagatctt gctgttgcct 120

tcaacgctgg tcaaatcaaa acaggctctt tatcacgttc tgagcgtgtt gcaaaataca 180

atagactcat ggaaattgaa gaagagcttg gatccgaagc aattttcaca gattctaatg 240

tattttctta cgaggattct gaggaataga gggattttct ctatttctat cttatctcca 300

aatcaagaat acatcgcaga tctatgggcc ttatctttc 339

<210> 44

<211> 60

<212> DNA

<213> Chlamydia pneumoniae

<400> 44
agcacaaatc caacagttgc tctcgcatca atatttgatg caaaaactac aaaatgtcca 60

<210> 45

<211> 165

<212> DNA

<213> Chlamydia pneumoniae

<400> 45
accgacatac tcgtcaaatt cattaagaac atcttcccac ccctgtggag aggtaatgtc 60

gtaccccgca gcaaaaatat gacaagtatc tacacacacg ccaatgggaa tttgattttt 120

caaattctga acgaggtaac ccaattcttc aaagttactc ccaat 165

<210> 46

<211> 78

<212> DNA

<213> Chlamydia pneumoniae

<400> 46
tcttctcgct gtacacaacg agaaattgct gggaggagaa cggtaaacac accaaagcca 60

aagagatgta tggggagc 78

<210> 47

<211> 384

<212> DNA

<213> Chlamydia pneumoniae

<400> 47
attgatgcca cccagatcaa ccttaatgcc tcccaagttg acattcacat taggaaccac 60

agtagctcct actggagtgc caggacctgt atgagacgtc gagtgagccc ctccacctgg 120

agtttcattt ataaaggaga agtctggagc tggggtcgtt ttccagttaa tgcctttcaa 180

gcccccaaca tcatcccaaa tcggacctgt ttctactttt gctccacgac gccatgcaga 240

gggtgtatat ccactactag attctttagc attccaagga ccgtagacta cagcagtttt 300

aaatttcatg ctgagcatca gatgattgta atttcctgtg gctcccgagc gctcttccat 360

tgtaggtttt acgcgtcccg tcca 384

<210> 48

<211> 147

<212> DNA

<213> Chlamydia pneumoniae

<400> 48
gccctttat cacgagcttg tgtggcatca atcataccag ctcgtaagtc cgcatcaatc 60
gccatctgtt tacctggcat cgcatccaat cggaatcggg cagcaacttc ggcaacacgc 120
tcggcaccct tagttactac gataaac 147

<210> 49
<211> 144
<212> DNA
<213> Chlamydia pneumoniae

<400> 49
aataaggtaa ttacaggatc atggcgagtg ggagcttgtg agagcatgga aaccagaaag 60
ccacctaaat gcttgaaaaa aaaggtcgat agggagaaag ccgtaaacat agagacgata 120
aaggtaaccg cagaaggaaa atcc 144

<210> 50
<211> 348
<212> DNA
<213> Chlamydia pneumoniae

<400> 50
ggcatctctg tgatgatgat gctctcacga tgtttatctt cattctcttc tacatgcaga 60
cgagctcgaa ctttaatctt tcctcgtcct gtagtatacg tggagcgaat tccttcagaa 120
ccgcagataa ttcctcctgt agggaaatca gggcctggca tgacttgtaa aatctcatcc 180
acagaagcct gtggatttgc aagcagaaga agtgtagctt ctataagttc ccctaaattg 240
tgtgggggga tattcgttgc catcccaaca gcaattcctg aagaaccatt gcaaagaaga 300
ttcggaaatt tagaaggaaa aactacaggc tcgtgttttg tttcatca 348

<210> 51
<211> 444
<212> DNA
<213> Chlamydia pneumoniae

<400> 51
agtggcagaa ttatctccgt catgttgtcc gctccaccgt gtgagctgca tagtgacttg 60
atagatcccg acttgtttga gtttaaccac aggctcaata tctgcatatc tgctgaagtc 120
aggggtcgcg ttacgactca cacttttaga ggtgatagct gcaacatgag tttcaattgt 180
agtgttaggg gcaacgtaat aaccattccc aggataatac gtatagagat tcgcagcctg 240

acatccagtt tttctataat aactaaatgt aagcgcatct cgagcagact gaggatcact 300
aatattattg catactggag tttgcgatac gtctgtctta gaatagatat taaaaccgtc 360
agagagtgta gtagcattaa gttgagaacc ttccgcagac acattaccct tcacaataaa 420
ttcacatgga gaagtcgtgg tatc 444

<210> 52
<211> 180
<212> DNA
<213> Chlamydia pneumoniae

<400> 52
agtgatcgta actctttttc aatctctgtg agtttttcaa aatacgcaga ttttatagca 60
cctctgaact ggagcttacg caccagaagg gcgttcaacc cagtagaagc cgccctcatt 120
cgattttcac attcttcaag agttaggcca gaagttactg ttccagaaat aaggaactca 180

<210> 53
<211> 189
<212> DNA
<213> Chlamydia pneumoniae

<400> 53
atgccttgga ttttctataa acttttcaat ataaacattg gggttattaa aaccggcttc 60
ggcttctgca cgtgcggcag aaaacgctct atagaattcg tccttttctt taacaatacg 120
aattcctctt cccccacctc cagcaacggc tttaataaca atagggaaac ctattttttc 180
agctatttt 189

<210> 54
<211> 255
<212> DNA
<213> Chlamydia pneumoniae

<400> 54
atttccatgt cttccataga aaccccttct tcaccgacaa cttccatacg cttgccgatt 60
tctgaacctt tctctagaaa ctgtgctgct tttttcacag caccacccca gcctgaaacc 120
ttctcttcta aaatttgtcc tacctggttc aaatattttg accaagaaat caaagggtct 180
attgaaggat acctacgtgc gtcagctcgt gcttttgaaa gaccacagaa cgctccgact 240
acagctaatg tagat 255

<210> 55

<211> 135

<212> DNA

<213> Chlamydia pneumoniae

<400> 55
ggagaccttg aacattataa acacatccat ggaccttttt caaaatcaag ccaccatggc 60

aaacgtcata agcgccacaa ttatttaatg ttcctacagt gtcgatataa gactctatgc 120

ggtgatcagg aatca 135

<210> 56

<211> 87

<212> DNA

<213> Chlamydia pneumoniae

<400> 56
agggtatctt tcaatgcatc cccgccgatc acaacaagtc gtagggactc caaacaggaa 60

ttttgttttt ttgctgtttt cagaata 87

<210> 57

<211> 258

<212> DNA

<213> Chlamydia pneumoniae

<400> 57
tcaataaacc cactagcacc acagcgttca ttaggccctg ccatacaata ccagctagaa 60

gaatggccga tacaggacac ttcgatttca cgagacccta agcgactttc ctccacaaac 120

acatccgtgt catatagaaa tgcttctgag atcttttctt gtaattcctc tttatcacgg 180

actaaaaata tcccaatact agatcccaaa tgtgcagttt ttacaatcat agggaaagaa 240

aatgtctcta taagattc 258

<210> 58

<211> 135

<212> DNA

<213> Chlamydia pneumoniae

<400> 58
ccactaggtc ccgcaccaat aacaacacaa tcaaattctt gggtcatatt ctcactcact 60
gtaatcaaga tttcaaaaag aacccccctt cataaatgca tgcatctcat taagaagagg 120
accctgtgct tattt 135

<210> 59
<211> 207
<212> DNA
<213> Chlamydia pneumoniae

<400> 59
ggagaacaac cattcctgtt tcatcccact tcacagcaaa gtttgtctct gtatcatcac 60
tatataggca ccctacaatc gtctttccat cactggaaac accctctgca aaagattgca 120
ttccctcaga aaatattcca agatcaacaa gtgcaccgtt tacccacttc acagcgcggc 180
aagacggatc ttgatccgag attccta 207

<210> 60
<211> 285
<212> DNA
<213> Chlamydia pneumoniae

<400> 60
gtgacatcta agtacgcttc catgcgtcca tcaattccta atccagcttc acatacacgt 60
aaaatagcac gcgctcctac atctcggctg acaagattcc catacgcagg atacatatct 120
tctaagaaat accaaggagc tcctgtctct ccacaaggac gttccgaacc atctggaaat 180
actatgcgct ttgaagaatc cccaggcacc cacacacgac cgccctcacc acgcacagac 240
tctgaaatta atcgtagctt atcccttcca ggaattgctg taggg 285

<210> 61
<211> 651
<212> PRT
<213> Chlamydia pneumoniae

<400> 61

Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr
1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn
20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305   310   315   320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
                325   330   335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
            340   345   350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
        355   360   365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
    370   375   380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385   390   395   400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
                405   410   415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
            420   425   430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
        435   440   445

Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val
    450   455   460

Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr
465   470   475   480

Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr
                485   490   495

Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser
            500   505   510

Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
        515   520   525

Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn
    530   535   540

Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser
545   550   555   560

Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile
                565   570   575

Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr
580 585 590

Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys
595 600 605

Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys
610 615 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val
625 630 635 640

Asn Ile Gly Ser Leu Tyr Ser Gly Tyr Leu Gln
645 650

<210> 62

<211> 389

<212> PRT

<213> Chlamydia pneumoniae

<400> 62

Met Lys Lys Leu Leu Lys Ser Ala Leu Leu Ser Ala Ala Phe Ala Gly
1 5 10 15

Ser Val Gly Ser Leu Gln Ala Leu Pro Val Gly Asn Pro Ser Asp Pro
20 25 30

Ser Leu Leu Ile Asp Gly Thr Ile Trp Glu Gly Ala Ala Gly Asp Pro
35 40 45

Cys Asp Pro Cys Ala Thr Trp Cys Asp Ala Ile Ser Leu Arg Ala Gly
50 55 60

Phe Tyr Gly Asp Tyr Val Phe Asp Arg Ile Leu Lys Val Asp Ala Pro
65 70 75 80

Lys Thr Phe Ser Met Gly Ala Lys Pro Thr Gly Ser Ala Ala Ala Asn
85 90 95

Tyr Thr Thr Ala Val Asp Arg Pro Asn Pro Ala Tyr Asn Lys His Leu
100 105 110

His Asp Ala Glu Trp Phe Thr Asn Ala Gly Phe Ile Ala Leu Asn Ile
115 120 125

Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr
130 135 140

Ile Arg Gly Asn Ser Thr Ala Phe Asn Leu Val Gly Leu Phe Gly Val
145 150 155 160

Lys Gly Thr Thr Val Asn Ala Asn Glu Leu Pro Asn Val Ser Leu Ser
165 170 175

Asn Gly Val Val Glu Leu Tyr Thr Asp Thr Ser Phe Ser Trp Ser Val
180 185 190

Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr Leu Gly Ala
195 200 205

Glu Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu Glu Leu Asn Val
210 215 220

Ile Cys Asn Val Ser Gln Phe Ser Val Asn Lys Pro Lys Gly Tyr Lys
225 230 235 240

Gly Val Ala Phe Pro Leu Pro Thr Asp Ala Gly Val Ala Thr Ala Thr
245 250 255

Gly Thr Lys Ser Ala Thr Ile Asn Tyr His Glu Trp Gln Val Gly Ala
260 265 270

Ser Leu Ser Tyr Arg Leu Asn Ser Leu Val Pro Tyr Ile Gly Val Gln
275 280 285

Trp Ser Arg Ala Thr Phe Asp Ala Asp Asn Ile Arg Ile Ala Gln Pro
290 295 300

Lys Leu Pro Thr Ala Val Leu Asn Leu Thr Ala Trp Asn Pro Ser Leu
305 310 315 320

Leu Gly Asn Ala Thr Ala Leu Ser Thr Thr Asp Ser Phe Ser Asp Phe
325 330 335

Met Gln Ile Val Ser Cys Gln Ile Asn Lys Phe Lys Ser Arg Lys Ala
340 345 350

Cys Gly Val Thr Val Gly Ala Thr Leu Val Asp Ala Asp Lys Trp Ser
355 360 365

Leu Thr Ala Glu Ala Arg Leu Ile Asn Glu Arg Ala Ala His Val Ser
370 375 380

Gly Gln Phe Arg Phe
385

<210> 63

<211> 213

<212> PRT

<213> Chlamydia pneumoniae

<400> 63

Met Ser Val Asn Pro Ser Gly Asn Ser Lys Asn Asp Leu Trp Ile Thr
1 5 10 15

Gly Ala His Asp Gln His Pro Asp Val Lys Glu Ser Gly Val Thr Ser
20 25 30

Ala Asn Leu Gly Ser His Arg Val Thr Ala Ser Gly Gly Arg Gln Gly
35 40 45

Leu Leu Ala Arg Ile Lys Glu Ala Val Thr Gly Phe Phe Ser Arg Met
50 55 60

Ser Phe Phe Arg Ser Gly Ala Pro Arg Gly Ser Gln Gln Pro Ser Ala
65 70 75 80

Pro Ser Ala Asp Thr Val Arg Ser Pro Leu Pro Gly Gly Asp Ala Arg
85 90 95

Ala Thr Glu Gly Ala Gly Arg Asn Leu Ile Lys Lys Gly Tyr Gln Pro
100 105 110

Gly Met Lys Val Thr Ile Pro Gln Val Pro Gly Gly Gly Ala Gln Arg
115 120 125

Ser Ser Gly Ser Thr Thr Leu Lys Pro Thr Arg Pro Ala Pro Pro Pro
130 135 140

Pro Lys Thr Gly Gly Thr Asn Ala Lys Arg Pro Ala Thr His Gly Lys
145 150 155 160

Gly Pro Ala Pro Gln Pro Pro Lys Thr Gly Gly Thr Asn Ala Lys Arg
165 170 175

Ala Ala Thr His Gly Lys Gly Pro Ala Pro Gln Pro Pro Lys Gly Ile
180 185 190

Leu Lys Gln Pro Gly Gln Ser Gly Thr Ser Gly Lys Lys Arg Val Ser
195 200 205

Trp Ser Asp Glu Asp
210

<210> 64

<211> 382

<212> PRT

<213> Chlamydia pneumoniae

<400> 64

Met Gly Ile Asn Pro Ser Gly Asn Arg Ser Pro Asp Asp Val Trp Val
1 5 10 15

Arg Gly Ala Gln Gly Asp Ser Ser Ser Thr Gln Gly Thr Gly Ala Thr
20 25 30

Asn Ser Asn Leu Gly Ala His Asn Val Thr Thr Ser Thr Ser Gln Pro
35 40 45

Gln Val Ala Ser Lys Ala Lys Gln Leu Trp Gln Thr Val Arg Glu Phe
50 55 60

Phe Leu Gly Lys Lys Ser Pro Asp Ser Ser Gln Gly Ala Ser Gly Pro
65 70 75 80

Ala Met Gln Ser Pro Ser Gly Pro Thr Ile Arg Pro Thr Arg Pro Ala
85 90 95

Pro Pro Pro Pro Thr Thr Gly Gly Ala Asn Ala Lys Arg Pro Ala Thr
100 105 110

His Gly Lys Gly Arg Ala Pro Gln Pro Pro Thr Ala Gly Ser Ser Ser
115 120 125

Gly Ser Glu Gln Pro Thr Ala Met Ser Ser Glu Val Ala Lys Leu Val
130 135 140

Ser Glu Leu Lys Asp Ala Val His Ser His Ala Glu Ser Gln Lys Val
145 150 155 160

Leu Lys Lys Val Ser Gln Glu Leu Gln Thr Lys Trp Thr Asp Trp Glu
165 170 175

Asn Asn Arg Gly Pro Asp Tyr Leu Leu His Gly Tyr Arg Val Ile Ala
180 185 190

Arg Ala Leu Gln Gln Thr Tyr Thr Glu Gln Ser Met Leu Ile Glu Gly
195 200 205

Thr Ser Ser Thr Gly Pro Val Pro Gln Ala Val Thr Val Ala Lys Asp
210 215 220

Ala Val Thr Gln Thr Val Arg Gly Ala Ile Lys Asn Leu Glu Asn Pro
225 230 235 240

Lys Pro Gly Asn Asp Pro Asp Gly Val Leu Met Gln Val Val Ile Ser
245 250 255

Leu Gly Ile Glu Gly Pro Thr Leu Asp Pro Gly Glu Ser Ile Gln Asn
260 265 270

Phe Leu Glu Thr Arg Val Ser Asp Phe Gly Gly Asp Asp Ser Asp Ile
275 280 285

Asp Tyr Thr Ser Asp Ile Ala Arg Leu Gly Ser Ala Leu Asp Arg Val
290 295 300

Arg Glu Asn His Pro Asn Glu Met Pro Arg Ile Trp Ile Ala Leu Ala
305 310 315 320

Arg Glu Leu Gly Ala Ala Val His Ser His Ala Thr Ser Val Arg Ile
325 330 335

Ala Asn Ala Gly Lys Asn His Thr Arg Asp Val Val Arg Met Ala Asn
340 345 350

Glu Ser Ser Arg Leu Leu Gln Gly Met Lys Val Leu Ser Val Gly Ala
355 360 365

Trp Ala Asn Thr Met Thr Val Leu Ile Gly Asp Leu Phe Glu
370 375 380

<210> 65

<211> 333

<212> PRT

<213> Chlamydia pneumoniae

<400> 65

Met Lys Thr Leu Trp His Phe Val Ser Lys Ala Phe Leu Ser Ile Val
1 5 10 15

Gly Leu Cys Cys Gly Val Val Leu Ala Phe Val Val Ile Phe Ala Leu
20 25 30

Ile Ala Ser Ser Leu Gly Asn Gly Asp Ala Thr Phe Val Ser Leu Pro
35 40 45

Asp Ala Gln Gly Glu Val Lys Asp Leu Gly Lys Thr Ala Pro Ile Ile
50 55 60

Ala Val Ile Glu Met Lys Asp Val Ile Ala Ser Ser Lys Asn Thr Ala
65 70 75 80

Lys Thr Ile Gln Asn Ile Leu Glu Gly Phe Glu Lys Ala Pro Leu Lys
85 90 95

Asp Arg Val Lys Gly Ile Val Ile Asp Met Asp Cys Pro Gly Gly Glu
100 105 110

Val Phe Glu Ile Asp Arg Ile Tyr Ser Met Leu Arg Phe Trp Lys Glu
115 120 125

Arg Lys Gly Phe Pro Ile Tyr Ile Tyr Val Asn Gly Leu Cys Ala Ser
130 135 140

Gly Gly Tyr Tyr Val Ser Cys Ala Ala Thr Lys Ile Tyr Ala Thr Ser
145 150 155 160

Ser Ser Leu Ile Gly Ser Ile Gly Val Arg Ser Gly Pro Phe Phe Asn
165 170 175

Val Lys Glu Gly Leu Asn Arg Tyr Gly Val Glu Ser Asp Leu Leu Thr
180 185 190

Ala Gly Lys Asp Lys Ala Pro Met Asn Pro Tyr Thr Pro Trp Thr Ser
195 200 205

His Asp Arg Glu Glu Arg Gln Ala Thr Leu Asp Phe Leu Tyr Gly Gln
210 215 220

Phe Val Asp Ile Val Thr Gln Asn Arg Pro Leu Leu Thr Lys Glu Lys
225 230 235 240

Leu Val His Thr Leu Gly Ala Arg Ile Phe Ser Pro Glu Lys Ala Lys
245 250 255

Gln Glu Gly Tyr Ile Asp Val Val Gly Ala Thr Lys Glu Gln Val Leu
260 265 270

Gln Asp Ile Val Ala Val Cys Lys Ile Glu Asp Asn Tyr Arg Val Ile
275 280 285

Gly Ser Gly Gly Asp Gly Trp Trp Lys Arg Val Ala Ser Ala Ala Ala
290 295 300

Ser Ser Pro Leu Val Thr Gly Met Ile Lys His Asp Ile Leu Pro Leu
305 310 315 320

Ser His Asp Ala Ala Tyr Ile Pro Pro Tyr Leu Ala Leu
325 330

<210> 66

<211> 228

<212> PRT

<213> Chlamydia pneumoniae

<400> 66

Met Arg Pro His Arg Lys His Val Ser Ser Lys Ser Leu Ala Leu Lys
1 5 10 15

Gln Ser Ala Ser Thr His Val Glu Ile Thr Thr Lys Ala Phe Arg Leu
20 25 30

Ser Met Pro Leu Lys Gln Leu Ile Leu Glu Lys Ser Asp His Leu Pro
35 40 45

Pro Met Glu Thr Ile Arg Val Val Leu Thr Ser His Lys Asp Lys Leu
50 55 60

Gly Thr Glu Val His Val Val Ala Ser His Gly Lys Glu Ile Leu Gln
65 70 75 80

Thr Lys Val His Asn Ala Asn Pro Tyr Thr Ala Val Ile Asn Ala Phe
85 90 95

Lys Lys Ile Arg Thr Met Ala Asn Lys His Ser Asn Lys Arg Lys Asp
100 105 110

Arg Thr Lys His Asp Leu Gly Leu Ala Ala Lys Glu Glu Arg Ile Ala
115 120 125

Ile Gln Glu Glu Gln Glu Asp Arg Leu Ser Asn Glu Trp Leu Pro Val
130 135 140

Glu Gly Leu Asp Ala Trp Asp Ser Leu Lys Thr Leu Gly Tyr Val Pro
145 150 155 160

Ala Ser Ala Lys Lys Lys Ile Ser Lys Lys Lys Met Ser Ile Arg Met
165 170 175

Leu Ser Gln Asp Glu Ala Ile Arg Gln Leu Glu Ser Ala Ala Glu Asn
180 185 190

Phe Leu Ile Phe Leu Asn Glu Gln Glu His Lys Ile Gln Cys Ile Tyr
195 200 205

Lys Lys His Asp Gly Asn Tyr Val Leu Ile Glu Pro Ser Leu Lys Pro
210 215 220

Gly Phe Cys Ile
225

<210> 67

<211> 755

<212> PRT

<213> Chlamydia pneumoniae

<400> 67

Met Ala Ala Pro Ile Asn Gln Pro Ser Thr Thr Thr Gln Ile Thr Gln
1   5   10   15

Thr Gly Gln Thr Thr Thr Thr Thr Thr Val Gly Ser Leu Gly Glu His
            20   25   30

Ser Val Thr Thr Thr Gly Ser Gly Ala Ala Ala Gln Thr Ser Gln Thr
        35   40   45

Val Thr Leu Ile Ala Asp His Glu Met Gln Glu Ile Ala Ser Gln Asp
    50   55   60

Gly Ser Ala Val Ser Phe Ser Ala Glu His Ser Phe Ser Thr Leu Pro
65   70   75   80

Pro Glu Thr Gly Ser Val Gly Ala Thr Ala Gln Ser Ala Gln Ser Ala
                85   90   95

Gly Leu Phe Ser Leu Ser Gly Arg Thr Gln Arg Arg Asp Ser Glu Ile
            100   105   110

Ser Ser Ser Ser Asp Gly Ser Ser Ile Ser Arg Thr Ser Ser Asn Ala
        115   120   125

Ser Ser Gly Glu Thr Ser Arg Ala Glu Ser Ser Pro Asp Leu Gly Asp
    130   135   140

Leu Asp Ser Leu Ser Gly Ser Glu Arg Ala Glu Gly Ala Glu Gly Pro
145   150   155   160

Glu Gly Pro Gly Gly Leu Pro Glu Ser Thr Ile Pro His Tyr Asp Pro
                165   170   175

Thr Asp Lys Ala Ser Ile Leu Asn Phe Leu Lys Asn Pro Ala Val Gln
            180   185   190

Gln Lys Met Gln Thr Lys Gly Gly His Phe Val Tyr Val Asp Glu Ala
        195   200   205

Arg Ser Ser Phe Ile Phe Val Arg Asn Gly Asp Trp Ser Thr Ala Glu
    210   215   220

Ser Ile Lys Val Ser Asn Ala Lys Thr Lys Glu Asn Ile Thr Lys Pro
225 230 235 240

Ala Asp Leu Glu Met Cys Ile Ala Lys Phe Cys Val Gly Tyr Glu Thr
245 250 255

Ile His Ser Asp Trp Thr Gly Arg Val Lys Pro Thr Met Glu Glu Arg
260 265 270

Ser Gly Ala Thr Gly Asn Tyr Asn His Leu Met Leu Ser Met Lys Phe
275 280 285

Lys Thr Ala Val Val Tyr Gly Pro Trp Asn Ala Lys Glu Ser Ser Ser
290 295 300

Gly Tyr Thr Pro Ser Ala Trp Arg Arg Gly Ala Lys Val Glu Thr Gly
305 310 315 320

Pro Ile Trp Asp Asp Val Gly Gly Leu Lys Gly Ile Asn Trp Lys Thr
325 330 335

Thr Pro Ala Pro Asp Phe Ser Phe Ile Asn Glu Thr Pro Gly Gly Gly
340 345 350

Ala His Ser Thr Ser His Thr Gly Pro Gly Thr Pro Val Gly Ala Thr
355 360 365

Val Val Pro Asn Val Asn Val Asn Leu Gly Gly Ile Lys Val Asp Leu
370 375 380

Gly Gly Ile Asn Leu Gly Gly Ile Thr Thr Asn Val Thr Thr Glu Glu
385 390 395 400

Gly Gly Gly Thr Asn Ile Thr Ser Thr Lys Ser Thr Ser Thr Asp Asp
405 410 415

Lys Val Ser Ile Thr Ser Thr Gly Ser Gln Ser Thr Ile Glu Glu Asp
420 425 430

Thr Ile Gln Phe Asp Asp Pro Gly Gln Gly Glu Asp Asp Asn Ala Ile
435 440 445

Pro Gly Thr Asn Thr Pro Pro Pro Pro Gly Pro Pro Pro Asn Leu Ser
450 455 460

Ser Ser Arg Leu Leu Thr Ile Ser Asn Ala Ser Leu Asn Gln Val Leu
465 470 475 480

Gln Asn Val Arg Gln His Leu Asn Thr Ala Tyr Asp Ser Asn Gly Asn
485 490 495

Ser Val Ser Asp Leu Asn Gln Asp Leu Gly Gln Val Val Lys Asn Ser
500 505 510

Glu Asn Gly Val Asn Phe Pro Thr Val Ile Leu Pro Lys Thr Thr Gly
515 520 525

Asp Thr Asp Pro Ser Gly Gln Ala Thr Gly Gly Val Thr Glu Gly Gly
530 535 540

Gly His Ile Arg Asn Ile Ile Gln Arg Asn Thr Gln Ser Thr Gly Gln
545 550 555 560

Ser Glu Gly Ala Thr Pro Thr Pro Gln Pro Thr Ile Ala Lys Ile Val
565 570 575

Thr Ser Leu Arg Lys Ala Asn Val Ser Ser Ser Ser Val Leu Pro Gln
580 585 590

Pro Gln Val Ala Thr Thr Ile Thr Pro Gln Ala Arg Thr Ala Ser Thr
595 600 605

Ser Thr Thr Ser Ile Gly Thr Gly Thr Glu Ser Thr Ser Thr Thr Ser
610 615 620

Thr Gly Thr Gly Thr Gly Ser Val Ser Thr Gln Ser Thr Gly Val Gly
625 630 635 640

Thr Pro Thr Thr Thr Thr Arg Ser Thr Gly Thr Ser Ala Thr Thr Thr
645 650 655

Thr Ser Ser Ala Ser Thr Gln Thr Pro Gln Ala Pro Leu Pro Ser Gly
660 665 670

Thr Arg His Val Ala Thr Ile Ser Leu Val Arg Asn Ala Ala Gly Arg
675 680 685

Ser Ile Val Leu Gln Gln Gly Gly Arg Ser Gln Ser Phe Pro Ile Pro
690 695 700

Pro Ser Gly Thr Gly Thr Gln Asn Met Gly Ala Gln Leu Trp Ala Ala
705 710 715 720

Ala Ser Gln Val Ala Ser Thr Leu Gly Gln Val Val Asn Gln Ala Ala
725 730 735

Thr Ala Gly Ser Gln Pro Ser Ser Arg Arg Ser Ser Pro Thr Ser Pro
740 745 750

Arg Arg Lys
755

<210> 68

<211> 568

<212> PRT

<213> Chlamydia pneumoniae

<400> 68

Met Lys Thr Ser Gln Leu Phe Tyr Lys Thr Ser Lys Asn Ala Asn Lys
1 5 10 15

Ser Ala Ala Val Leu Ser Asn Glu Leu Leu Glu Lys Ala Gly Tyr Leu
20 25 30

Phe Lys Val Ser Lys Gly Val Tyr Thr Tyr Thr Pro Leu Leu Trp Arg
35 40 45

Val Val Ser Lys Met Met Asn Ile Ile Arg Glu Glu Leu Asn Ala Ile
50 55 60

Gly Gly Gln Glu Leu Leu Leu Pro Leu Leu His Asn Ala Glu Leu Trp
65 70 75 80

Gln His Thr Gly Arg Trp Glu Ala Phe Thr Ser Glu Gly Leu Leu Tyr
85 90 95

Thr Leu Lys Asp Arg Glu Gly Lys Ser His Cys Leu Ala Pro Thr His
100 105 110

Glu Glu Val Ile Cys Ser Phe Val Ala Gln Trp Leu Ser Ser Lys Arg
115 120 125

Gln Leu Pro Leu His Leu Tyr Gln Ile Ala Thr Lys Phe Arg Asp Glu
130 135 140

Ile Arg Pro Arg Phe Gly Leu Ile Arg Ser Arg Glu Leu Leu Met Glu
145 150 155 160

Asp Ser Tyr Thr Phe Ser Asp Ser Pro Glu Gln Met Asn Glu Gln Tyr
165 170 175

Glu Lys Leu Arg Ser Ala Tyr Ser Lys Ile Phe Asp Arg Leu Gly Leu
180 185 190

Ala Tyr Val Ile Val Thr Ala Asp Gly Gly Lys Ile Gly Lys Gly Lys
195 200 205

Ser Glu Glu Phe Gln Val Leu Cys Ser Leu Gly Glu Asp Thr Ile Cys
210 215 220

Val Ser Gly Ser Tyr Gly Ala Asn Ile Glu Ala Ala Val Ser Ile Pro
225 230 235 240

Pro Gln His Ala Tyr Asp Arg Glu Phe Leu Pro Val Glu Glu Val Ala
245 250 255

Thr Pro Gly Ile Thr Thr Ile Glu Ala Leu Ala Asn Phe Phe Ser Ile
260 265 270

Pro Leu His Lys Ile Leu Lys Thr Leu Val Val Lys Leu Ser Tyr Ser
275 280 285

Asn Glu Glu Lys Phe Ile Ala Ile Gly Met Arg Gly Asp Arg Gln Val
290 295 300

Asn Leu Val Lys Val Ala Ser Lys Leu Asn Ala Asp Asp Ile Ala Leu
305 310 315 320

Ala Ser Asp Glu Glu Ile Glu Arg Val Leu Gly Thr Glu Lys Gly Phe
325 330 335

Ile Gly Pro Leu Asn Cys Pro Ile Asp Phe Phe Ala Asp Glu Thr Thr
340 345 350

Ser Pro Met Thr Asn Phe Val Cys Ala Gly Asn Ala Lys Asp Lys His
355 360 365

Tyr Val Asn Val Asn Trp Asp Arg Asp Leu Leu Pro Pro Gln Tyr Gly
370 375 380

Asp Phe Leu Leu Ala Glu Glu Gly Asp Thr Cys Pro Glu Asn Pro Gly
385 390 395 400

His Pro Tyr Arg Ile Tyr Gln Gly Ile Glu Val Ala His Ile Phe Asn
405 410 415

Leu Gly Thr Arg Tyr Thr Asp Ser Phe Glu Val Asn Phe Gln Asp Glu
420 425 430

His Gly Gln Thr Gln Gln Cys Trp Met Gly Thr Tyr Gly Ile Gly Val
435 440 445

Gly Arg Thr Leu Ala Ala Cys Val Glu Gln Leu Ala Asp Asp Arg Gly
450 455 460

Ile Val Trp Pro Lys Ala Leu Ala Pro Phe Ser Ile Thr Ile Ala Phe
465 470 475 480

Asn Gly Gly Asp Thr Val Ser Gln Glu Leu Ala Glu Thr Ile Tyr His
485 490 495

Glu Leu Gln Ser Gln Gly Tyr Glu Pro Leu Leu Asp Asp Arg Asp Glu
500 505 510

Arg Leu Gly Phe Lys Leu Lys Asp Ser Asp Leu Ile Gly Ile Pro Tyr
515 520 525

Lys Leu Ile Leu Gly Lys Ser Tyr Gln Ser Ser Gly Ile Phe Glu Ile
530 535 540

Glu Ser Arg Ser Gly Glu Lys Tyr Thr Val Ser Pro Glu Ala Phe Pro
545 550 555 560

Thr Trp Cys Gln Asn His Leu Ala
565

<210> 69

<211> 775

<212> PRT

<213> Chlamydia pneumoniae

<400> 69

Met Ala Ser Gly Ile Gly Gly Ser Ser Gly Leu Gly Lys Ile Pro Pro
1 5 10 15

Lys Asp Asn Gly Asp Arg Ser Arg Ser Pro Ser Pro Lys Gly Glu Leu
20 25 30

Gly Ser His Glu Ile Ser Leu Pro Pro Gln Glu His Gly Glu Glu Gly
35 40 45

Ala Ser Gly Ser Ser His Ile His Ser Ser Ser Ser Phe Leu Pro Glu
50 55 60

Asp Gln Glu Ser Gln Ser Ser Ser Ser Ala Ala Ser Ser Pro Gly Phe
65 70 75 80

Phe Ser Arg Val Arg Ser Gly Val Asp Arg Ala Leu Lys Ser Phe Gly
85 90 95

Asn Phe Phe Ser Ala Glu Ser Thr Ser Gln Ala Arg Glu Thr Arg Gln
100 105 110

Ala Phe Val Arg Leu Ser Lys Thr Ile Thr Ala Asp Glu Arg Arg Asp
115 120 125

Val Asp Ser Ser Ser Ala Ala Ala Thr Glu Ala Arg Val Ala Glu Asp
130 135 140

Ala Ser Val Ser Gly Glu Asn Pro Ser Gln Gly Val Pro Glu Thr Ser
145 150 155 160

Ser Gly Pro Glu Pro Gln Arg Leu Phe Ser Leu Pro Ser Val Lys Lys
165 170 175

Gln Ser Gly Leu Gly Arg Leu Val Gln Thr Val Arg Asp Arg Ile Val
180 185 190

Leu Pro Ser Gly Ala Pro Pro Thr Asp Ser Glu Pro Leu Ser Leu Tyr
195 200 205

Glu Leu Asn Leu Arg Leu Ser Ser Leu Arg Gln Glu Leu Ser Asp Ile
210 215 220

Gln Ser Asn Asp Gln Leu Thr Pro Glu Glu Lys Ala Glu Ala Thr Val
225 230 235 240

Thr Ile Gln Gln Leu Ile Gln Ile Thr Glu Phe Gln Cys Gly Tyr Met
245 250 255

Glu Ala Thr Gln Ser Ser Val Ser Leu Ala Glu Ala Arg Phe Lys Gly
260 265 270

Val Glu Thr Ser Asp Glu Ile Asn Ser Leu Cys Ser Glu Leu Thr Asp
275 280 285

Pro Glu Leu Gln Glu Leu Met Ser Asp Gly Asp Ser Leu Gln Asn Leu
290 295 300

Leu Asp Glu Thr Ala Asp Asp Leu Glu Ala Ala Leu Ser His Ala Arg
305 310 315 320

Leu Ser Phe Ser Leu Asp Asp Asn Pro Thr Pro Ile Asp Asn Asn Pro
325 330 335

Thr Leu Ile Ser Gln Glu Glu Pro Ile Tyr Glu Glu Ile Gly Gly Ala
340 345 350

Ala Asp Pro Gln Arg Thr Arg Glu Asn Trp Ser Thr Arg Leu Trp Asn
355 360 365

Gln Ile Arg Glu Ala Leu Val Ser Leu Leu Gly Met Ile Leu Ser Ile
370 375 380

Leu Gly Ser Ile Leu His Arg Leu Arg Ile Ala Arg His Ala Ala Ala
385 390 395 400

Glu Ala Val Gly Arg Cys Cys Thr Cys Arg Gly Glu Glu Cys Thr Ser
405 410 415

Ser Glu Glu Asp Ser Met Ser Val Gly Ser Pro Ser Glu Ile Asp Glu
420 425 430

Thr Glu Arg Thr Gly Ser Pro His Asp Val Pro Arg Arg Asn Gly Ser
435 440 445

Pro Arg Glu Asp Ser Pro Leu Met Asn Ala Leu Val Gly Trp Ala His
450 455 460

Lys His Gly Ala Lys Thr Lys Glu Ser Ser Glu Ser Ser Thr Pro Glu
465 470 475 480

Ile Ser Ile Ser Ala Pro Ile Val Arg Gly Trp Ser Gln Asp Ser Ser
485 490 495

Val Ser Phe Ile Val Met Glu Asp Asp His Ile Phe Tyr Asp Val Pro
500 505 510

Arg Arg Lys Asp Gly Ile Tyr Asp Val Pro Ser Ser Pro Arg Trp Ser
515 520 525

Pro Ala Arg Glu Leu Glu Glu Asp Val Phe Gly Asp Tyr Glu Val Pro
530 535 540

Ile Thr Ser Ala Glu Pro Ser Lys Asp Lys Asn Ile Tyr Met Thr Pro
545 550 555 560

Arg Leu Ala Thr Pro Ala Ile Tyr Asp Leu Pro Ser Arg Pro Gly Ser
565 570 575

Ser Gly Ser Ser Arg Ser Pro Ser Ser Asp Arg Val Arg Ser Ser Ser
580 585 590

Pro Asn Arg Arg Gly Val Pro Leu Pro Pro Val Pro Ser Pro Ala Met
595 600 605

Ser Glu Glu Gly Ser Ile Tyr Glu Asp Met Ser Gly Ala Ser Gly Ala
610 615 620

Gly Glu Ser Asp Tyr Glu Asp Met Ser Arg Ser Pro Ser Pro Arg Gly
625 630 635 640

Asp Leu Asp Glu Pro Ile Tyr Ala Asn Thr Pro Glu Asp Asn Pro Phe
645 650 655

Thr Gln Arg Asn Ile Asp Arg Ile Leu Gln Glu Arg Ser Gly Gly Ala
660 665 670

Ser Ala Ser Pro Val Glu Pro Ile Tyr Asp Glu Ile Pro Trp Ile His
675 680 685

Gly Arg Pro Pro Ala Thr Leu Pro Arg Pro Glu Asn Thr Leu Thr Asn
690 695 700

Val Ser Leu Arg Val Ser Pro Gly Phe Gly Pro Glu Val Arg Ala Ala
705 710 715 720

Leu Leu Ser Glu Ser Val Ser Ala Val Met Val Glu Ala Glu Ser Ile
725 730 735

Val Pro Pro Thr Glu Pro Gly Asp Gly Glu Ser Glu Tyr Leu Glu Pro
740 745 750

Leu Gly Gly Leu Val Ala Thr Thr Lys Ile Leu Leu Gln Lys Gly Trp
755 760 765

Pro Arg Gly Glu Ser Asn Ala
770 775

<210> 70

<211> 938

<212> PRT

<213> Chlamydia pneumoniae

<400> 70

Met Arg Phe Phe Cys Phe Gly Met Leu Leu Pro Phe Thr Phe Val Leu
1 5 10 15

Ala Asn Glu Gly Leu Gln Leu Pro Leu Glu Thr Tyr Ile Thr Leu Ser
20 25 30

Pro Glu Tyr Gln Ala Ala Pro Gln Val Gly Phe Thr His Asn Gln Asn
35 40 45

Gln Asp Leu Ala Ile Val Gly Asn His Asn Asp Phe Ile Leu Asp Tyr
50 55 60

Lys Tyr Tyr Arg Ser Asn Gly Gly Ala Leu Thr Cys Lys Asn Leu Leu
65 70 75 80

Ile Ser Glu Asn Ile Gly Asn Val Phe Phe Glu Lys Asn Val Cys Pro
85 90 95

Asn Ser Gly Gly Ala Ile Tyr Ala Ala Gln Asn Cys Thr Ile Ser Lys
100 105 110

Asn Gln Asn Tyr Ala Phe Thr Thr Asn Leu Val Ser Asp Asn Pro Thr
115 120 125

Ala Thr Ala Gly Ser Leu Leu Gly Gly Ala Leu Phe Ala Ile Asn Cys
130 135 140

Ser Ile Thr Asn Asn Leu Gly Gln Gly Thr Phe Val Asp Asn Leu Ala
145 150 155 160

Leu Asn Lys Gly Gly Ala Leu Tyr Thr Glu Thr Asn Leu Ser Ile Lys
165 170 175

Asp Asn Lys Gly Pro Ile Ile Ile Lys Gln Asn Arg Ala Leu Asn Ser
180 185 190

Asp Ser Leu Gly Gly Gly Ile Tyr Ser Gly Asn Ser Leu Asn Ile Glu
195 200 205

Gly Asn Ser Gly Ala Ile Gln Ile Thr Ser Asn Ser Ser Gly Ser Gly
210 215 220

Gly Gly Ile Phe Ser Thr Gln Thr Leu Thr Ile Ser Ser Asn Lys Lys
225 230 235 240

Leu Ile Glu Ile Ser Glu Asn Ser Ala Phe Ala Asn Asn Tyr Gly Ser
245 250 255

Asn Phe Asn Pro Gly Gly Gly Gly Leu Thr Thr Thr Phe Cys Thr Ile
260 265 270

Leu Asn Asn Arg Glu Gly Val Leu Phe Asn Asn Asn Gln Ser Gln Ser
275 280 285

Asn Gly Gly Ala Ile His Ala Lys Ser Ile Ile Ile Lys Glu Asn Gly
290 295 300

Pro Val Tyr Phe Leu Asn Asn Thr Ala Thr Arg Gly Gly Ala Leu Leu
305 310 315 320

Asn Leu Ser Ala Gly Ser Gly Asn Gly Ser Phe Ile Leu Ser Ala Asp
325 330 335

Asn Gly Asp Ile Ile Phe Asn Asn Asn Thr Ala Ser Lys His Ala Leu
340 345 350

Asn Pro Pro Tyr Arg Asn Ala Ile His Ser Thr Pro Asn Met Asn Leu
355 360 365

Gln Ile Gly Ala Arg Pro Gly Tyr Arg Val Leu Phe Tyr Asp Pro Ile
370 375 380

Glu His Glu Leu Pro Ser Ser Phe Pro Ile Leu Phe Asn Phe Glu Thr
385 390 395 400

Gly His Thr Gly Thr Val Leu Phe Ser Gly Glu His Val His Gln Asn
405 410 415

Phe Thr Asp Glu Met Asn Phe Phe Ser Tyr Leu Arg Asn Thr Ser Glu
420 425 430

Leu Arg Gln Gly Val Leu Ala Val Glu Asp Gly Ala Gly Leu Ala Cys
435 440 445

Tyr Lys Phe Phe Gln Arg Gly Gly Thr Leu Leu Leu Gly Gln Gly Ala
450 455 460

Val Ile Thr Thr Ala Gly Thr Ile Pro Thr Pro Ser Ser Thr Pro Thr
465 470 475 480

Thr Val Gly Ser Thr Ile Thr Leu Asn His Ile Ala Ile Asp Leu Pro
485 490 495

Ser Ile Leu Ser Phe Gln Ala Gln Ala Pro Lys Ile Trp Ile Tyr Pro
500 505 510

Thr Lys Thr Gly Ser Thr Tyr Thr Glu Asp Ser Asn Pro Thr Ile Thr
515 520 525

Ile Ser Gly Thr Leu Thr Leu Arg Asn Ser Asn Asn Glu Asp Pro Tyr
530 535 540

Asp Ser Leu Asp Leu Ser His Ser Leu Glu Lys Val Pro Leu Leu Tyr
545 550 555 560

Ile Val Asp Val Ala Ala Gln Lys Ile Asn Ser Ser Gln Leu Asp Leu
565 570 575

Ser Thr Leu Asn Ser Gly Glu His Tyr Gly Tyr Gln Gly Ile Trp Ser
580 585 590

Thr Tyr Trp Val Glu Thr Thr Thr Ile Thr Asn Pro Thr Ser Leu Leu
595 600 605

Gly Ala Asn Thr Lys His Lys Leu Leu Tyr Ala Asn Trp Ser Pro Leu
610 615 620

Gly Tyr Arg Pro His Pro Glu Arg Arg Gly Glu Phe Ile Thr Asn Ala
625 630 635 640

Leu Trp Gln Ser Ala Tyr Thr Ala Leu Ala Gly Leu His Ser Leu Ser
645 650 655

Ser Trp Asp Glu Glu Lys Gly His Ala Ala Ser Leu Gln Gly Ile Gly
660 665 670

Leu Leu Val His Gln Lys Asp Lys Asn Gly Phe Lys Gly Phe Arg Ser
675 680 685

His Met Thr Gly Tyr Ser Ala Thr Thr Glu Ala Thr Ser Ser Gln Ser
690 695 700

Pro Asn Phe Ser Leu Gly Phe Ala Gln Phe Phe Ser Lys Ala Lys Glu
705 710 715 720

His Glu Ser Gln Asn Ser Thr Ser Ser His His Tyr Phe Ser Gly Met
725 730 735

Cys Ile Glu Asn Thr Leu Phe Lys Glu Trp Ile Arg Leu Ser Val Ser
740 745 750

Leu Ala Tyr Met Phe Thr Ser Glu His Thr His Thr Met Tyr Gln Gly
755 760 765

Leu Leu Glu Gly Asn Ser Gln Gly Ser Phe His Asn His Thr Leu Ala
770 775 780

Gly Ala Leu Ser Cys Val Phe Leu Pro Gln Pro His Gly Glu Ser Leu
785 790 795 800

Gln Ile Tyr Pro Phe Ile Thr Ala Leu Ala Ile Arg Gly Asn Leu Ala
805 810 815

Ala Phe Gln Glu Ser Gly Asp His Ala Arg Glu Phe Ser Leu His Arg
820 825 830

Pro Leu Thr Asp Val Ser Leu Pro Val Gly Ile Arg Ala Ser Trp Lys
835 840 845

Asn His His Arg Val Pro Leu Val Trp Leu Thr Glu Ile Ser Tyr Arg
850 855 860

Ser Thr Leu Tyr Arg Gln Asp Pro Glu Leu His Ser Lys Leu Leu Ile
865 870 875 880

Ser Gln Gly Thr Trp Thr Thr Gln Ala Thr Pro Val Thr Tyr Asn Ala
885 890 895

Leu Gly Ile Lys Val Lys Asn Thr Met Gln Val Phe Pro Lys Val Thr
900 905 910

Leu Ser Leu Asp Tyr Ser Ala Asp Ile Ser Ser Ser Thr Leu Ser His
915 920 925

Tyr Leu Asn Val Ala Ser Arg Met Arg Phe
930 935

<210> 71

<211> 928

<212> PRT

<213> Chlamydia pneumoniae

<400> 71

Met Lys Ser Ser Leu His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu
1 5 10 15

Pro Leu Ser Leu Asn Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn
20 25 30

Leu Gly Pro Thr Asn Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro
35 40 45

Ala Gln Thr Thr Asn Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp
50 55 60

Val Ser Ile Thr Asn Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys
65 70 75 80

Phe Lys Glu Thr Thr Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln
85 90 95

Phe Leu Leu Gln Asn Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn
100 105 110

Thr Ala Ala Asn Lys Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser
115 120 125

Leu Ile Gln Thr Thr Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser
130 135 140

Thr Gly Ala Cys Ser Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln
145 150 155 160

Asn Phe Ser Asn Asp Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser
165 170 175

Leu Ser Leu Asn Pro Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln
180 185 190

Lys Gly Gly Ala Leu Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr
195 200 205

Leu Asn Ser Ala Ser Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly
210 215 220

Ala Ile Tyr Thr Glu Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile
225 230 235 240

Ser Phe Ile Asn Asn Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala
245 250 255

Ile Tyr Cys Ser Ser Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser
260 265 270

Asp Asn Gly Glu Leu Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly
275 280 285

Gly Ala Ile Tyr Thr Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr
290 295 300

Leu Phe Lys Asn Asn Ser Ala Ile Asp Thr Ala Ala Pro Leu Gly Gly
305 310 315 320

Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly
325 330 335

Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser
340 345 350

Ser Gln Thr Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala
355 360 365

Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr
370 375 380

Asp Pro Ile Thr Thr Ser Ile Thr Ala Ala Leu Ser Asp Ala Leu Asn
385 390 395 400

Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile
405 410 415

Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp
420 425 430

Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln
435 440 445

Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln
450 455 460

Ser Pro Gly Ser Thr Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr
465 470 475 480

Ala Asp Gly Ile Thr Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu
485 490 495

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Lys Glu Thr Lys Lys Ala Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr
            500                 505                 510

Val Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val
        515                 520                 525

Tyr Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr
    530                 535                 540

Leu Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala
545                 550                 555                 560

Asp Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp
                565                 570                 575

Ala Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr
            580                 585                 590

Leu Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly
        595                 600                 605

Thr Leu Val Ala Asn Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser
    610                 615                 620

Ile Gln Gln Leu Val Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg
625                 630                 635                 640

Gly Ile Trp Cys Glu Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr
                645                 650                 655

Lys Ile Asn Lys Gly Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly
            660                 665                 670

Ala Thr Thr Thr Leu Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys
        675                 680                 685

Gln Leu Phe Gly Lys Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala
    690                 695                 700

Ser Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser
705                 710                 715                 720

Ser Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro
                725                 730                 735

Val Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met
            740                 745                 750

Lys Thr Tyr Tyr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn
        755                 760                 765
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Asp Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu
770 775 780

Ser His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu
785 790 795 800

Ala Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu
805 810 815

Val Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile
820 825 830

Gly Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu
835 840 845

Ala Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys
850 855 860

Thr Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr
865 870 875 880

Asn Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala
885 890 895

Phe Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg
900 905 910

Gly Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe
915 920 925

<210> 72

<211> 845

<212> PRT

<213> Chlamydia pneumoniae

<400> 72

Met Phe Glu Lys Phe Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala
1 5 10 15

Lys Lys Glu Ala Gln Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His
20 25 30

Ile Leu Leu Gly Leu Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val
35 40 45

Leu Arg Asn Leu Gly Ile Asp Phe Asp Thr Ala Arg Gln Glu Val Glu
50 55 60

Arg Leu Ile Gly Tyr Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala
65   70   75   80

Leu Thr Gly Arg Val Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala
                85   90   95

Ser Leu Leu Glu His Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly
            100   105   110

Ile Leu His Gln Ser Asp Ser Val Ala Leu Gln Val Leu Glu Asn Leu
        115   120   125

His Ile Asp Pro Arg Glu Val Arg Lys Glu Ile Leu Lys Glu Leu Glu
    130   135   140

Thr Phe Asn Leu Gln Leu Pro Pro Ser Ser Ser Ser Ser Ser Ser Ser
145   150   155   160

Ser Arg Ser Asn Pro Ser Ser Ser Lys Ser Pro Leu Gly His Ser Leu
                165   170   175

Gly Ser Asp Lys Asn Glu Lys Leu Ser Ala Leu Lys Ala Tyr Gly Tyr
            180   185   190

Asp Leu Thr Glu Met Val Arg Glu Ser Lys Leu Asp Pro Val Ile Gly
        195   200   205

Arg Ser Ser Glu Val Glu Arg Leu Ile Leu Ile Leu Cys Arg Arg Arg
    210   215   220

Lys Asn Asn Pro Val Leu Ile Gly Glu Ala Gly Val Gly Lys Thr Ala
225   230   235   240

Ile Val Glu Gly Leu Ala Gln Lys Ile Ile Leu Asn Glu Val Pro Asp
                245   250   255

Ala Leu Arg Lys Lys Arg Leu Ile Thr Leu Asp Leu Ala Leu Met Ile
            260   265   270

Ala Gly Thr Lys Tyr Arg Gly Gln Phe Glu Glu Arg Ile Lys Ala Val
        275   280   285

Met Asp Glu Val Arg Lys His Gly Asn Ile Leu Leu Phe Ile Asp Glu
    290   295   300

Leu His Thr Ile Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala
305   310   315   320

Ser Asn Ile Leu Lys Pro Ala Leu Ala Arg Gly Glu Ile Gln Cys Ile
                325   330   335

Gly Ala Thr Thr Ile Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala
340 345 350

Ala Leu Glu Arg Arg Phe Gln Lys Ile Val Val His Pro Pro Ser Val
355 360 365

Asp Glu Thr Ile Glu Ile Leu Arg Gly Leu Lys Lys Lys Tyr Glu Glu
370 375 380

His His Asn Val Phe Ile Thr Glu Glu Ala Leu Lys Ala Ala Ala Thr
385 390 395 400

Leu Ser Asp Gln Tyr Val His Gly Arg Phe Leu Pro Asp Lys Ala Ile
405 410 415

Asp Leu Leu Asp Glu Ala Gly Ala Arg Val Arg Val Asn Thr Met Gly
420 425 430

Gln Pro Thr Asp Leu Met Lys Leu Glu Ala Glu Ile Glu Asn Thr Lys
435 440 445

Leu Ala Lys Glu Gln Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala
450 455 460

Gly Leu Arg Asp Glu Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met
465 470 475 480

Lys Gln Glu Trp Glu Asn His Lys Glu Glu His Gln Val Pro Val Asp
485 490 495

Glu Glu Ala Val Ala Gln Val Val Ser Leu Gln Thr Gly Ile Pro Ser
500 505 510

Ala Arg Leu Thr Glu Ala Glu Ser Glu Lys Leu Leu Lys Leu Glu Asp
515 520 525

Thr Leu Arg Arg Lys Val Ile Gly Gln Asn Asp Ala Val Thr Ser Ile
530 535 540

Cys Arg Ala Ile Arg Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg
545 550 555 560

Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Ser
565 570 575

Leu Leu Ala Gln Gln Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ala
580 585 590

Leu Ile Gln Val Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr
595 600 605

Lys Met Met Gly Ser Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly
610 615 620

His Leu Thr Glu Gln Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe
625 630 635 640

Asp Glu Ile Glu Lys Ala His Pro Asp Ile Met Asp Leu Met Leu Gln
645 650 655

Ile Leu Glu Gln Gly Arg Leu Thr Asp Ser Phe Gly Arg Lys Val Asp
660 665 670

Phe Arg His Ala Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu
675 680 685

Ile Arg Lys Ser Gly Glu Ile Gly Phe Gly Leu Lys Ser His Met Asp
690 695 700

Tyr Lys Val Ile Gln Glu Lys Ile Glu His Ala Met Lys Lys His Leu
705 710 715 720

Lys Pro Glu Phe Ile Asn Arg Leu Asp Glu Ser Val Ile Phe Arg Pro
725 730 735

Leu Glu Lys Glu Ser Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys
740 745 750

Leu Asp Ser Arg Leu Lys Asn Tyr Gln Met Ala Leu Asn Ile Pro Asp
755 760 765

Ser Val Ile Ser Phe Leu Val Thr Lys Gly His Ser Pro Glu Met Gly
770 775 780

Ala Arg Pro Leu Arg Arg Val Ile Glu Gln Tyr Leu Glu Asp Pro Leu
785 790 795 800

Ala Glu Leu Leu Leu Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu
805 810 815

Arg Ala Thr Leu Val Glu Asn Arg Val Ala Phe Glu Arg Glu Glu Glu
820 825 830

Glu Gln Glu Ala Ala Leu Pro Ser Pro His Leu Glu Ser
835 840 845

<210> 73

<211> 404

<212> PRT

<213> Chlamydia pneumoniae

<400> 73

Met Gly Leu Gln Ser Arg Leu Gln His Cys Ile Glu Val Ser Gln Asn
1   5   10   15

Ser Asn Phe Asp Ser Gln Val Lys Gln Phe Ile Tyr Ala Cys Gln Asp
            20   25   30

Lys Thr Leu Arg Gln Ser Val Leu Lys Ile Phe Arg Tyr His Pro Leu
        35   40   45

Leu Lys Ile His Asp Ile Ala Arg Ala Val Tyr Leu Leu Met Ala Leu
    50   55   60

Glu Glu Gly Glu Asp Leu Gly Leu Ser Phe Leu Asn Val Gln Gln Tyr
65   70   75   80

Pro Ser Gly Ala Val Glu Leu Phe Ser Cys Gly Gly Phe Pro Trp Lys
                85   90   95

Gly Leu Pro Tyr Pro Ala Glu His Ala Glu Phe Gly Leu Leu Leu Leu
            100   105   110

Gln Ile Ala Glu Phe Tyr Glu Glu Ser Gln Ala Tyr Val Ser Lys Met
        115   120   125

Ser His Phe Gln Gln Ala Leu Phe Asp His Gln Gly Ser Val Phe Pro
    130   135   140

Ser Leu Trp Ser Gln Glu Asn Ser Arg Leu Leu Lys Glu Lys Thr Thr
145   150   155   160

Leu Ser Gln Ser Phe Leu Phe Gln Leu Gly Met Gln Ile His Pro Glu
                165   170   175

Tyr Ser Leu Glu Asp Pro Ala Leu Gly Phe Trp Met Gln Arg Thr Arg
            180   185   190

Ser Ser Ser Ala Phe Val Ala Ala Ser Gly Cys Gln Ser Ser Leu Gly
        195   200   205

Ala Tyr Ser Ser Gly Asp Val Gly Val Ile Ala Tyr Gly Pro Cys Ser
    210   215   220

Gly Asp Ile Ser Asp Cys Tyr Tyr Phe Gly Cys Cys Gly Ile Ala Lys
225   230   235   240

Glu Phe Val Cys Gln Lys Ser His Gln Thr Thr Glu Ile Ser Phe Leu
                245   250   255

Thr Ser Thr Gly Lys Pro His Pro Arg Asn Thr Gly Phe Ser Tyr Leu
260 265 270

Arg Asp Ser Tyr Val His Leu Pro Ile Arg Cys Lys Ile Thr Ile Ser
275 280 285

Asp Lys Gln Tyr Arg Val His Ala Ala Leu Ala Glu Ala Thr Ser Ala
290 295 300

Met Thr Phe Ser Ile Phe Cys Lys Gly Lys Asn Cys Gln Val Val Asp
305 310 315 320

Gly Pro Arg Leu Arg Ser Cys Ser Leu Asp Ser Tyr Lys Gly Pro Gly
325 330 335

Asn Asp Ile Met Ile Leu Gly Glu Asn Asp Ala Ile Asn Ile Val Ser
340 345 350

Ala Ser Pro Tyr Met Glu Ile Phe Ala Leu Gln Gly Lys Glu Lys Phe
355 360 365

Trp Asn Ala Asp Phe Leu Ile Asn Ile Pro Tyr Lys Glu Glu Gly Val
370 375 380

Met Leu Ile Phe Glu Lys Lys Val Thr Ser Glu Lys Gly Arg Phe Phe
385 390 395 400

Thr Lys Met Asn

<210> 74

<211> 369

<212> PRT

<213> Chlamydia pneumoniae

<400> 74

Met Thr Lys Ile Ala Phe Ser Glu Lys Ala Lys Asn Phe Pro Val Glu
1 5 10 15

Ala Leu Lys Lys Trp Phe Glu Lys Asn Lys Arg Ser Leu Pro Trp Arg
20 25 30

Asp Asn Pro Thr Pro Tyr Ser Val Trp Val Ser Glu Val Met Leu Gln
35 40 45

Gln Thr Arg Ala Glu Val Val Ile Asp Tyr Phe Asn Gln Trp Met Glu
50 55 60

Arg Phe Pro Thr Ile Glu Ser Leu Ala Ala Ala Lys Glu Glu Asp Val
65 70 75 80

Ile Lys Leu Trp Glu Gly Leu Gly Tyr Tyr Ser Arg Ala Arg His Leu
85 90 95

Leu Glu Gly Ala Arg Met Val Met Glu Glu Phe His Gly Lys Ile Pro
100 105 110

Asp Asp Ala Ile Ser Leu Ala Gln Ile Arg Gly Val Gly Pro Tyr Thr
115 120 125

Val His Ala Ile Leu Ala Phe Ala Phe Lys Arg Arg Ala Ala Ala Val
130 135 140

Asp Gly Asn Val Leu Arg Val Leu Ser Arg Ile Phe Leu Ile Glu Thr
145 150 155 160

Ser Ile Asp Leu Glu Ser Thr Arg Thr Trp Val Ser Arg Ile Ala Gln
165 170 175

Ala Leu Leu Pro His Lys Ser Pro Glu Val Ile Ala Glu Ala Leu Ile
180 185 190

Glu Leu Gly Ala Cys Ile Cys Lys Lys Val Pro Gln Cys His Arg Cys
195 200 205

Pro Val Arg Gln Ala Cys Gly Ala Trp Arg Glu Asn Lys Gln Phe Val
210 215 220

Leu Pro Val Arg His Ala Arg Lys Lys Val Ile Phe Leu His Arg Leu
225 230 235 240

Val Ala Ile Val Leu Tyr Asp Gly Ser Leu Val Val Glu Lys Arg Arg
245 250 255

Pro Lys Glu Met Met Ala Gly Leu Tyr Glu Phe Pro Tyr Ile Glu Val
260 265 270

Glu Pro Glu Glu Gly Leu Gln Asp Ile Glu Gly Phe Thr Lys Lys Met
275 280 285

Glu Leu Ser Leu Glu Ser Pro Leu Glu Phe Leu Gly Asn Leu Lys Glu
290 295 300

Gln Arg His Ala Phe Thr Asn His Lys Val His Leu Cys Pro Ile Ile
305 310 315 320

Phe Lys Ala Thr Ser Leu Pro Gln Phe Gly Glu Leu His Leu Leu Ser
325 330 335

Asp Ile Asp His Leu Ala Phe Ser Ser Gly His Lys Lys Ile Lys Asp
340 345 350

Ala Leu Leu Ile Tyr Leu Gly Asp Val Arg Ser Arg Glu Ser Ile Gly
355 360 365

Val

<210> 75

<211> 579

<212> PRT

<213> Chlamydia pneumoniae

<400> 75

Met Ala Val Ser Gly Gly Gly Gly Val Gln Pro Ser Ser Asp Pro Gly
1 5 10 15

Lys Trp Asn Pro Ala Leu Gln Gly Glu Gln Ala Glu Gly Pro Ser Pro
20 25 30

Leu Lys Glu Ser Ile Phe Ser Glu Thr Lys Gln Ala Ser Ser Ala Ala
35 40 45

Lys Gln Glu Ser Leu Val Arg Ser Gly Ser Thr Gly Met Tyr Ala Thr
50 55 60

Glu Ser Gln Ile Asn Lys Ala Lys Tyr Arg Lys Ala Gln Asp Arg Ser
65 70 75 80

Ser Thr Ser Pro Lys Ser Lys Leu Lys Gly Thr Phe Ser Lys Met Arg
85 90 95

Ala Ser Val Gln Gly Phe Met Ser Gly Phe Gly Ser Arg Ala Ser Arg
100 105 110

Val Ser Ala Lys Arg Ala Ser Asp Ser Gly Glu Gly Thr Ser Leu Leu
115 120 125

Pro Thr Glu Met Asp Val Ala Leu Lys Lys Gly Asn Arg Ile Ser Pro
130 135 140

Glu Met Gln Gly Phe Phe Leu Asp Ala Ser Gly Met Gly Gly Ser Ser
145 150 155 160

Ser Asp Ile Ser Gln Leu Ser Leu Glu Ala Leu Lys Ser Ser Ala Phe
165 170 175

Ser Gly Ala Arg Ser Leu Ser Leu Ser Ser Ser Glu Ser Ser Ser Val
180 185 190

Ala Ser Phe Gly Ser Phe Gln Lys Ala Ile Glu Pro Met Ser Glu Glu
195 200 205

Lys Val Asn Ala Trp Thr Val Ala Arg Leu Gly Gly Glu Met Val Ser
210 215 220

Ser Leu Leu Asp Pro Asn Val Glu Thr Ser Ser Leu Val Arg Arg Ala
225 230 235 240

Met Ala Thr Gly Asn Glu Gly Met Ile Asp Leu Ser Asp Leu Gly Gln
245 250 255

Glu Glu Val Ser Thr Ala Met Thr Ser Pro Arg Ala Val Glu Gly Lys
260 265 270

Val Lys Val Ser Ser Ser Asp Ser Pro Glu Ala Asn Pro Thr Gly Ile
275 280 285

Pro Asn Ser Asn Thr Leu Glu Arg Ala Glu Lys Glu Ala Glu Lys Gln
290 295 300

Glu Ser Arg Glu Gln Leu Ser Glu Asp Gln Met Met Leu Ala Arg Ala
305 310 315 320

Met Ala Gly Leu Leu Thr Gly Ala Ala Pro Gln Glu Val Leu Ser Asn
325 330 335

Ser Val Trp Ser Gly Pro Ser Thr Val Phe Pro Pro Pro Lys Phe Ser
340 345 350

Gly Thr Leu Pro Thr Gln Arg Ser Gly Asp Lys Ser Lys His Lys Ser
355 360 365

Pro Gly Ile Glu Lys Ser Thr Asn His Thr Asn Phe Ser Pro Leu Arg
370 375 380

Glu Gly Thr Val Lys Ser Ala Glu Val Lys Ser Leu Pro His Pro Glu
385 390 395 400

Ser Met Tyr Arg Phe Pro Lys Asp Ser Ile Val Ser Arg Glu Glu Pro
405 410 415

Glu Ala Val Val Lys Glu Ser Thr Ala Phe Lys Asn Pro Glu Asn Ser
420 425 430

Ser Gln Asn Phe Leu Pro Ile Ala Val Glu Ser Val Phe Pro Lys Glu
435 440 445

Ser Gly Thr Gly Gly Ala Leu Gly Ser Asp Ala Val Ser Ser Ser Tyr
450 455 460

His Phe Leu Ala Gln Arg Gly Val Ser Leu Leu Ala Pro Leu Pro Arg
465 470 475 480

Ala Thr Asp Asp Tyr Lys Glu Lys Leu Glu Ala His Lys Gly Pro Gly
485 490 495

Gly Pro Pro Asp Pro Leu Ile Tyr Gln Tyr Arg Asn Val Ala Val Glu
500 505 510

Pro Pro Ile Val Leu Arg Ser Pro Gln Pro Phe Ser Gly Ser Ser Arg
515 520 525

Leu Ser Val Gln Gly Lys Pro Glu Ala Ala Ser Val His Asp Asp Gly
530 535 540

Gly Gly Gly Asn Ser Gly Gly Phe Ser Gly Asp Gln Arg Arg Gly Ser
545 550 555 560

Ser Gly Gln Lys Ala Ser Arg Gln Glu Lys Lys Gly Lys Lys Leu Ser
565 570 575

Thr Asp Ile

<210> 76

<211> 1142

<212> PRT

<213> Chlamydia pneumoniae

<220>

<221> MISC_FEATURE

<222> (1023)..(1023)

<223> X may be any amino acid

<400> 76

Met Lys Arg Arg Ser Trp Leu Lys Ile Leu Gly Ile Cys Leu Gly Ser
1 5 10 15

Ser Ile Val Leu Gly Phe Leu Ile Phe Leu Pro Gln Leu Leu Ser Thr
20 25 30

Glu Ser Gly Lys Tyr Leu Val Phe Ser Leu Ile His Lys Glu Ser Gly
35 40 45

Leu Ser Cys Ser Ala Glu Glu Leu Lys Ile Ser Trp Phe Gly Arg Gln
50 55 60

Thr Ala Arg Lys Ile Lys Leu Thr Gly Glu Ala Lys Asp Glu Val Phe
65 70 75 80

Ser Ala Glu Lys Phe Glu Leu Asp Gly Ser Leu Leu Arg Leu Leu Ile
85 90 95

Tyr Lys Lys Pro Lys Gly Ile Thr Leu Ser Gly Trp Ser Leu Lys Ile
100 105 110

Asn Glu Pro Ala Ser Ile Asp His Pro Ser Val Ser His Leu Asp Pro
115 120 125

Gly Ser Leu Leu Thr Tyr Leu Asn Asp Cys Lys Ile Ile Ser Glu His
130 135 140

Gly Phe Ile Thr Met Lys Thr Val Ser Gly Ser Ser Leu Ser Val Ser
145 150 155 160

Gly Phe Tyr Leu Glu Lys Ser Ser Glu Lys Phe Met Thr Lys Cys Val
165 170 175

Val Ser Glu Asp Gln Gln Ser Gly Asn Ile Phe Ile Glu Ser Val Leu
180 185 190

Ser Pro Asp Val Ser Ile Ser Ala Gln Phe Ser Ser Val Pro Val Ala
195 200 205

Phe Phe Lys Ile Phe Ile Ala Ser Pro Phe Trp Asp His Leu Leu Ser
210 215 220

Tyr Glu Asp Ile Ile Asn Leu Ser Ala Glu Ala Thr His Thr Asn Asp
225 230 235 240

Gly Lys Ile Ser Met Thr Ala Ser Gly Glu Gly Asn Gln Ile Gln Met
245 250 255

Lys Leu Gln Gly His Ile His Lys Ser Thr Phe Tyr Ile Val Glu Gly
260 265 270

Ser Ser Ser Phe Ile Glu Leu Lys Pro Glu Leu Ala Ser Ala Leu Cys
275 280 285

Asn Gln Ile Ile Pro Leu Ser Thr Pro Ile Thr Ser Lys Gln Ile His
290 295 300

Ala Thr Val Ser Tyr Ala Lys Ile Pro Leu Asp Ile Thr Lys Trp Lys
305 310 315 320

His Ile Glu Ile Thr Ser Gln Ala Gln Leu Pro Glu Val Ala Ile His
325 330 335

Pro Lys Asp Pro Asn Leu Ala Leu Gln Leu Arg Asp Thr Lys Leu Gly
340 345 350

Ile Lys Lys Thr Glu Lys Phe Ser Asp Ile Arg Tyr Ser Ser Ser Thr
355 360 365

Val Leu Gly Gly Ala Ser Pro Ser His Leu Asn Gly Leu Ile Ser Ile
370 375 380

Asp Asn Lys Lys His Leu Thr Lys Phe Arg Leu Gln Gln Ala Gln Leu
385 390 395 400

Pro His Thr Tyr Leu Arg Ala Ile Phe Pro Gln Pro Phe Val Ile Asn
405 410 415

Val Pro Leu Asp Val Ala Tyr Tyr Ser Leu Asn Ile Glu Gly Thr Tyr
420 425 430

Lys Asn Ala His Leu Glu Ala Asp Ala Ile Leu Asp Asn Pro Leu Leu
435 440 445

Lys Leu Ser Cys Ser Met Ser Gly Ala Trp Lys Asn Phe Leu Phe Lys
450 455 460

Gly Gln Gly Thr Tyr His Phe Asn Lys Lys Trp Gln Glu Ile Leu Ser
465 470 475 480

Pro His Phe Ser Tyr Ala Glu Ala Arg Phe Ser Gly Lys Ala Gln Ile
485 490 495

Thr Asp Thr Asn Leu Phe Phe Pro Lys Phe Ser Gly Lys Ile Thr Ala
500 505 510

Arg Glu Asn Glu Leu Leu Ile His Ala Lys Phe Gly Ser Pro Asn Glu
515 520 525

Pro Ile Lys Pro Glu Thr Thr Ser Ile Leu Ile His Gly Gln Phe Cys
530 535 540

Ser Leu Pro Leu Ser Leu Val Ser Asn His Leu Ala Pro Phe His Leu
545 550 555 560

Lys Lys Leu Thr Phe Ser Phe His Thr Asp Gly Gly Lys Phe Val Thr
565 570 575

Lys Gly Asn Leu Gln Ala Leu Ile Glu Asn Pro Asp Tyr Pro Asp Leu
580 585 590

Asn Asn Thr Arg Ile Leu Ile Pro Asp Leu Leu Leu Ser Leu Asp Glu
595 600 605

Ser Ser Thr Ser Pro Ser Ser Lys Asp Leu Lys Ile Gln Gly Ser Gly
610 615 620

Glu Ile Phe Ser Leu Pro Leu Asp Ser Ile Thr Lys Thr Tyr Gly Lys
625 630 635 640

Gln Val Arg Leu Ser Pro Tyr Phe Gly Ser Ser Gly Asp Leu Asn Phe
645 650 655

Val Val Asn Tyr Asn Pro Lys Asp Gln Asn Lys Leu Thr Leu Leu Ser
660 665 670

Asn Phe Lys Ser Glu Ala Leu Leu Gly Glu Leu Lys Leu Val Met Asp
675 680 685

Phe Ser Met Lys Leu Ser Ser Gly Thr Gln Gly Thr Leu Gln Trp Glu
690 695 700

Val Ser Pro Glu Arg Tyr Ala Ser Phe Phe Lys Asn Ala Ser Cys Ser
705 710 715 720

Pro Thr Cys Leu Leu His Arg Thr Ala Asn Val Arg Leu Asp Ile Ser
725 730 735

Lys Leu Ser Cys Pro Glu Glu Thr Lys Gly Leu Ser Cys Leu Thr Leu
740 745 750

Leu Ala Ala Gly Gly Leu Glu Gly Ser Leu Glu Ala Thr Pro Leu Ile
755 760 765

Phe Tyr Asp Asn Val Ser Lys Glu Thr Phe Ile Ile Asn Asp Phe Lys
770 775 780

Gly Ser Leu Arg Ala Asn Asn Leu Asp Ala Lys Ile Glu Tyr Asp Leu
785 790 795 800

Lys Gly Ser Cys Leu Ala Pro Arg Gln Asp Ser Lys Thr Leu Ala Glu
805 810 815

Phe Ser Leu Glu Gly Gln Val Asp His Leu Phe Ser Pro Glu Ser Arg
820 825 830

Glu Phe Lys Gln Thr Ala Asn Trp Ile His Ile Pro Ser Ser Phe Ile
835 840 845

Ala Gly Ile Ile Pro Met Ser Pro Gly Leu Lys Ala Gln Ile Ser Ser
850 855 860

Leu Ala Gly Pro Arg Ile Asn Val Ser Ile Lys Asn Ala Phe Arg Phe
865 870 875 880

Gly Glu Gly Pro Val Asp Ile Met Val Asp Ser Glu Asn Leu Gln Ala
885 890 895

Gln Ile Pro Leu Ile Leu Asn Glu Lys Ser Ile Leu Leu Arg Glu Asn
900 905 910

Leu Thr Ala His Leu Ser Ile Asn Glu Asp Val Asn Lys Ala Phe Leu
915 920 925

Gln Glu Phe Asn Pro Leu Leu Ala Gly Gly Ala Tyr Ser Gln Tyr Pro
930 935 940

Val Thr Leu Glu Ile Asp Lys Gln Asn Phe Tyr Leu Pro Ile Arg Pro
945 950 955 960

Tyr Ser Phe Glu Glu Phe Arg Ile Gln Ser Ala Thr Leu Asp Met Gly
965 970 975

Lys Ile Ser Ile Ala Asn Thr Gly Thr Met Tyr Ala Leu Phe Gln Phe
980 985 990

Leu Asp Ile Thr Asp Gln Lys Gln Phe Val Glu Ser Trp Phe Thr Pro
995 1000 1005

Ile Phe Phe Ser Val Gln Lys Gly Ser Ile Ile Cys Lys Arg Xaa
1010 1015 1020

Asp Ala Leu Ile Asp Arg Arg Ile Arg Leu Ala Leu Trp Gly Lys
1025 1030 1035

Thr Asp Ile Ala His Asp Arg Leu Phe Met Thr Leu Gly Ile Asp
1040 1045 1050

Pro Glu Val Ile Lys Lys Tyr Phe His Asn Thr Ser Leu Lys Thr
1055 1060 1065

Lys Asn Phe Phe Leu Ile Lys Ile Arg Gly Ser Ile Ser Ser Pro
1070 1075 1080

Glu Val Asp Trp Ser Ser Ala Tyr Ala Arg Ile Ala Leu Leu Lys
1085 1090 1095

Ser Tyr Ser Leu Gly Asn Pro Phe Ser Ser Leu Ala Asp Lys Leu
1100 1105 1110

Phe Ser Ser Leu Gly Asp Ser Thr Pro Pro Pro Thr Val His Pro
1115 1120 1125

Phe Pro Trp Glu Lys Ser Asn Phe Asp Ser Ile Glu Asn Lys
1130 1135 1140

<210> 77

<211> 390

<212> PRT

<213> Chlamydia pneumoniae

<400> 77

Met Ser Ser Pro Val Asn Asn Thr Pro Ser Ala Pro Asn Ile Pro Ile
1 5 10 15

Pro Ala Pro Thr Thr Pro Gly Ile Pro Thr Thr Lys Pro Arg Ser Ser
20 25 30

Phe Ile Glu Lys Val Ile Ile Val Ala Lys Tyr Ile Leu Phe Ala Ile
35 40 45

Ala Ala Thr Ser Gly Ala Leu Gly Thr Ile Leu Gly Leu Ser Gly Ala
50 55 60

Leu Thr Pro Gly Ile Gly Ile Ala Leu Leu Val Ile Phe Phe Val Ser
65 70 75 80

Met Val Leu Leu Gly Leu Ile Leu Lys Asp Ser Ile Ser Gly Gly Glu
85 90 95

Glu Arg Arg Leu Arg Glu Glu Val Ser Arg Phe Thr Ser Glu Asn Gln
100 105 110

Arg Leu Thr Val Ile Thr Thr Thr Leu Glu Thr Glu Val Lys Asp Leu
115 120 125

Lys Ala Ala Lys Asp Gln Leu Thr Leu Glu Ile Glu Ala Phe Arg Asn
130 135 140

Glu Asn Gly Asn Leu Lys Thr Thr Ala Glu Asp Leu Glu Glu Gln Val
145 150 155 160

Ser Lys Leu Ser Glu Gln Leu Glu Ala Leu Glu Arg Ile Asn Gln Leu
165 170 175

Ile Gln Ala Asn Ala Gly Asp Ala Gln Glu Ile Ser Ser Glu Leu Lys
180 185 190

Lys Leu Ile Ser Gly Trp Asp Ser Lys Val Val Glu Gln Ile Asn Thr
195 200 205

Ser Ile Gln Ala Leu Lys Val Leu Leu Gly Gln Glu Trp Val Gln Glu
210 215 220

Ala Gln Thr His Val Lys Ala Met Gln Glu Gln Ile Gln Ala Leu Gln
225 230 235 240

Ala Glu Ile Leu Gly Met His Asn Gln Ser Thr Ala Leu Gln Lys Ser
245 250 255

Val Glu Asn Leu Leu Val Gln Asp Gln Ala Leu Thr Arg Val Val Gly
260 265 270

Glu Leu Leu Glu Ser Glu Asn Lys Leu Ser Gln Ala Cys Ser Ala Leu
275 280 285

Arg Gln Glu Ile Glu Lys Leu Ala Gln His Glu Thr Ser Leu Gln Gln
290 295 300

Arg Ile Asp Ala Met Leu Ala Gln Glu Gln Asn Leu Ala Glu Gln Val
305 310 315 320

Thr Ala Leu Glu Lys Met Lys Gln Glu Ala Gln Lys Ala Glu Ser Glu
325 330 335

Phe Ile Ala Cys Val Arg Asp Arg Thr Phe Gly Arg Arg Glu Thr Pro
340 345 350

Pro Pro Thr Thr Pro Val Val Glu Gly Asp Glu Ser Gln Glu Glu Asp
355 360 365

Glu Gly Gly Thr Pro Pro Val Ser Gln Pro Ser Ser Pro Val Asp Arg
370 375 380

Ala Thr Gly Asp Gly Gln
385 390

<210> 78

<211> 820

<212> PRT

<213> Chlamydia pneumoniae

<400> 78

Met Arg Tyr Asp Pro Asn Leu Ile Glu Lys Lys Trp Gln Gln Phe Trp
1 5 10 15

Lys Glu His Arg Ser Phe Gln Ala Asn Glu Asp Glu Asp Lys Val Lys
20 25 30

Tyr Tyr Val Leu Asp Met Phe Pro Tyr Pro Ser Gly Ala Gly Leu His
35 40 45

Val Gly His Leu Ile Gly Tyr Thr Ala Thr Asp Ile Val Ala Arg Tyr
50 55 60

Lys Arg Ala Arg Gly Phe Ser Val Leu His Pro Met Gly Trp Asp Ser
65 70 75 80

Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Arg Thr Gly Thr His Pro
85 90 95

Lys Val Thr Thr Gln Lys Asn Ile Ala Asn Phe Lys Lys Gln Leu Ser
100 105 110

Ala Met Gly Phe Ser Tyr Asp Glu Gly Arg Glu Phe Ala Thr Ser Asp
115 120 125

Pro Asp Tyr Tyr His Trp Thr Gln Lys Leu Phe Leu Phe Leu Tyr Asp
130 135 140

Gln Gly Leu Ala Tyr Met Ala Asp Met Ala Val Asn Tyr Cys Pro Glu
145 150 155 160

Leu Gly Thr Val Leu Ser Asn Glu Glu Val Glu Asn Gly Phe Ser Ile
165 170 175

Glu Gly Gly Tyr Pro Val Glu Arg Lys Met Leu Arg Gln Trp Ile Leu
180 185 190

Lys Ile Thr Ala Tyr Ala Asp Lys Leu Leu Glu Gly Leu Asp Ala Leu
195 200 205

Asp Trp Pro Glu Asn Val Lys Gln Leu Gln Lys Asn Trp Ile Gly Lys
210 215 220

Ser Glu Gly Ala Leu Val Thr Phe His Leu Thr Gln Glu Gly Ser Leu
225 230 235 240

Glu Ala Phe Thr Thr Arg Leu Asp Thr Leu Leu Gly Val Ser Phe Leu
245 250 255

Val Ile Ala Pro Glu His Pro Asp Leu Asp Ser Ile Val Ser Glu Glu
260 265 270

Gln Arg Asp Glu Val Thr Ala Tyr Val Gln Glu Ser Leu Arg Lys Ser
275 280 285

Glu Arg Asp Arg Ile Ser Ser Val Lys Thr Lys Thr Gly Val Phe Thr
290 295 300

Gly Asn Tyr Ala Lys His Pro Ile Thr Gly Asn Leu Leu Pro Val Trp
305 310 315 320

Ile Ser Asp Tyr Val Val Leu Gly Tyr Gly Thr Gly Val Val Met Gly
325 330 335

Val Pro Ala His Asp Glu Arg Asp Arg Glu Phe Ala Glu Met Phe Ser
340 345 350

Leu Pro Ile His Glu Val Ile Asp Asp Asn Gly Val Cys Ile His Ser
355 360 365

Asn Tyr Asn Asp Phe Cys Leu Asn Gly Leu Ser Gly Gln Glu Ala Lys
370 375 380

Asp Tyr Val Ile Asn Tyr Leu Glu Met Arg Ser Leu Gly Arg Ala Lys
385 390 395 400

Thr Met Tyr Arg Leu Arg Asp Trp Leu Phe Ser Arg Gln Arg Tyr Trp
405 410 415

Gly Glu Pro Ile Pro Ile Ile His Phe Glu Asp Gly Thr His Arg Pro
420 425 430

Leu Glu Asp Asp Glu Leu Pro Leu Leu Pro Pro Asn Ile Asp Asp Tyr
435 440 445

Arg Pro Glu Gly Phe Gly Gln Gly Pro Leu Ala Lys Ala Gln Asp Trp
450 455 460

Val His Ile Tyr Asp Glu Lys Thr Gly Arg Pro Gly Cys Arg Glu Thr
465 470 475 480

Tyr Thr Met Pro Gln Trp Ala Gly Ser Cys Trp Tyr Tyr Leu Arg Phe
485 490 495

Cys Asp Ala His Asn Ser Gln Leu Pro Trp Ser Lys Glu Lys Glu Ser
500 505 510

Tyr Trp Met Pro Val Asp Leu Tyr Ile Gly Gly Ala Glu His Ala Val
515 520 525

Leu His Leu Leu Tyr Ser Arg Phe Trp His Arg Val Phe Tyr Asp Ala
530 535 540

Gly Leu Val Ser Thr Pro Glu Pro Phe Lys Lys Leu Ile Asn Gln Gly
545 550 555 560

Leu Val Leu Ala Ser Ser Tyr Arg Ile Pro Gly Lys Gly Tyr Val Ser
565 570 575

Ile Glu Asp Val Arg Glu Glu Asn Gly Thr Trp Ile Ser Thr Cys Gly
580 585 590

Glu Ile Val Glu Val Arg Gln Glu Lys Met Ser Lys Ser Lys Leu Asn
595 600 605

Gly Val Asp Pro Gln Val Leu Ile Glu Glu Tyr Gly Ala Asp Ala Leu
610 615 620

Arg Met Tyr Ala Met Phe Ser Gly Pro Leu Asp Lys Asn Lys Thr Trp
625 630 635 640

Ser Asn Glu Gly Val Gly Gly Cys Arg Arg Phe Leu Asn Arg Phe Tyr
645 650 655

Asp Leu Val Thr Ser Ser Glu Val Gln Asp Ile Glu Asp Arg Asp Gly
660 665 670

Leu Val Leu Ala His Lys Leu Val Phe Arg Ile Thr Glu His Ile Glu
675 680 685

Lys Met Ser Leu Asn Thr Ile Pro Ser Ser Phe Met Glu Phe Leu Asn
690 695 700

Asp Phe Ser Lys Leu Pro Val Tyr Ser Lys Arg Ala Leu Ser Met Ala
705 710 715 720

Val Arg Val Leu Glu Pro Ile Ala Pro His Ile Ser Glu Glu Leu Trp
725 730 735

Val Ile Leu Gly Asn Pro Pro Gly Ile Asp Gln Ala Ala Trp Pro Gln
740 745 750

Ile Asp Glu Ser Tyr Leu Val Ala Gln Thr Val Thr Phe Val Val Gln
755 760 765

Val Asn Gly Lys Leu Arg Gly Arg Leu Glu Val Ala Lys Glu Ala Pro
770 775 780

Lys Glu Glu Val Leu Ser Leu Ser Arg Ser Val Val Ala Lys Tyr Leu
785 790 795 800

Glu Asn Ala Gln Ile Arg Lys Glu Ile Tyr Val Pro Asn Lys Leu Val
805 810 815

Asn Phe Val Leu
820

<210> 79

<211> 1397

<212> PRT

<213> Chlamydia pneumoniae

<400> 79

Leu Glu Lys Ile Met Phe Gly Glu Asn Ser Arg Asp Ile Gly Val Leu
1   5   10   15

Ser Lys Glu Gly Leu Phe Asp Lys Leu Glu Ile Gly Ile Ala Ser Asp
            20   25   30

Ile Thr Ile Arg Asp Lys Trp Ser Cys Gly Glu Ile Lys Lys Pro Glu
        35   40   45

Thr Ile Asn Tyr Arg Thr Phe Lys Pro Glu Lys Gly Gly Leu Phe Cys
    50   55   60

Glu Lys Ile Phe Gly Pro Thr Lys Asp Trp Glu Cys Cys Cys Gly Lys
65   70   75   80

Tyr Lys Lys Ile Lys His Lys Gly Ile Val Cys Asp Arg Cys Gly Val
                85   90   95

Glu Val Thr Leu Ser Lys Val Arg Arg Glu Arg Met Ala His Ile Glu
            100   105   110

Leu Ala Val Pro Ile Val His Ile Trp Phe Phe Lys Thr Thr Pro Ser
        115   120   125

Arg Ile Gly Asn Val Leu Gly Met Thr Ala Ser Asp Leu Glu Arg Val
    130   135   140

Ile Tyr Tyr Glu Glu Tyr Val Val Ile Asp Pro Gly Lys Thr Asp Leu
145   150   155   160

Thr Lys Lys Gln Leu Leu Asn Asp Ala Gln Tyr Arg Glu Val Val Glu
                165   170   175

Lys Trp Gly Lys Asp Ala Phe Val Ala Lys Met Gly Gly Glu Ala Ile
            180   185   190

Tyr Asp Leu Leu Lys Ser Glu Asp Leu Gln Ser Leu Leu Lys Asp Leu
        195   200   205

Lys Glu Arg Leu Arg Lys Thr Lys Ser Gln Gln Ala Arg Met Lys Leu
    210   215   220

Ala Lys Arg Leu Lys Ile Ile Glu Gly Phe Val Ser Ser Ser Asn His
225 230 235 240

Pro Glu Trp Met Val Leu Lys Asn Ile Pro Val Val Pro Pro Asp Leu
245 250 255

Arg Pro Leu Val Pro Leu Asp Gly Gly Arg Phe Ala Thr Ser Asp Leu
260 265 270

Asn Asp Leu Tyr Arg Arg Val Ile Asn Arg Asn Asn Arg Leu Lys Ala
275 280 285

Ile Leu Arg Leu Lys Thr Pro Glu Val Ile Val Arg Asn Glu Lys Arg
290 295 300

Met Leu Gln Glu Ala Val Asp Ala Leu Phe Asp Asn Gly Arg His Gly
305 310 315 320

His Pro Val Met Gly Ala Gly Asn Arg Pro Leu Lys Ser Leu Ser Glu
325 330 335

Met Leu Lys Gly Lys Asn Gly Arg Phe Arg Gln Asn Leu Leu Gly Lys
340 345 350

Arg Val Asp Tyr Ser Gly Arg Ser Val Ile Ile Val Gly Pro Glu Leu
355 360 365

Lys Phe Asn Gln Cys Gly Leu Pro Lys Glu Met Ala Leu Glu Leu Phe
370 375 380

Glu Pro Phe Ile Ile Lys Arg Leu Lys Asp Gln Gly Ser Val Tyr Thr
385 390 395 400

Ile Arg Ser Ala Lys Lys Met Ile Gln Arg Gly Ala Pro Glu Val Trp
405 410 415

Asp Val Leu Glu Glu Ile Ile Lys Gly His Pro Val Leu Leu Asn Arg
420 425 430

Ala Pro Thr Leu His Arg Leu Gly Ile Gln Ala Phe Glu Pro Val Leu
435 440 445

Ile Glu Gly Lys Ala Ile Arg Ile His Pro Leu Val Cys Ala Ala Phe
450 455 460

Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu Ser
465 470 475 480

Val Glu Ala Gln Leu Glu Ala Lys Val Leu Met Met Ala Pro Asp Asn
485 490 495

Ile Phe Leu Pro Ser Ser Gly Lys Pro Val Ala Ile Pro Ser Lys Asp
500 505 510

Met Thr Leu Gly Leu Tyr Tyr Leu Met Ala Asp Pro Thr Tyr Phe Pro
515 520 525

Glu Glu His Gly Gly Lys Thr Lys Ile Phe Lys Asp Glu Ile Glu Val
530 535 540

Leu Arg Ala Leu Asn Asn Gly Gly Phe Ile Asp Asp Val Phe Gly Asp
545 550 555 560

Arg Arg Asp Glu Thr Gly Arg Gly Ile His Ile His Glu Lys Ile Lys
565 570 575

Val Arg Ile Asp Gly Gln Ile Ile Glu Thr Thr Pro Gly Arg Val Leu
580 585 590

Phe Asn Arg Ile Val Pro Lys Glu Leu Gly Phe Gln Asn Tyr Ser Met
595 600 605

Pro Ser Lys Arg Ile Ser Glu Leu Ile Leu Gln Cys Tyr Lys Lys Val
610 615 620

Gly Leu Glu Ala Thr Val Arg Phe Leu Asp Asp Leu Lys Asp Leu Gly
625 630 635 640

Phe Ile Gln Ala Thr Lys Ala Ala Ile Ser Met Gly Leu Lys Asp Val
645 650 655

Arg Ile Pro Asp Ile Lys Ser His Ile Leu Lys Asp Ala Tyr Asp Lys
660 665 670

Val Ala Ile Val Lys Lys Gln Tyr Asp Asp Gly Ile Ile Thr Glu Gly
675 680 685

Glu Arg His Ser Lys Thr Ile Ser Ile Trp Thr Glu Val Ser Glu Gln
690 695 700

Leu Ser Asp Ala Leu Tyr Val Glu Ile Ser Lys Gln Thr Arg Ser Lys
705 710 715 720

His Asn Pro Leu Phe Leu Met Ile Asp Ser Gly Ala Arg Gly Asn Lys
725 730 735

Ser Gln Leu Lys Gln Leu Gly Ala Leu Arg Gly Leu Met Ala Lys Pro
740 745 750

Asn Gly Ala Ile Ile Glu Ser Pro Ile Thr Ser Asn Phe Arg Glu Gly
755 760 765

Leu Thr Val Leu Glu Tyr Ser Ile Ser Ser His Gly Ala Arg Lys Gly
770 775 780

Leu Ala Asp Thr Ala Leu Lys Thr Ala Asp Ser Gly Tyr Leu Thr Arg
785 790 795 800

Arg Leu Val Asp Val Ala Gln Asp Val Ile Ile Thr Glu Lys Asp Cys
805 810 815

Gly Thr Leu Asn His Ile Glu Ile Ser Ala Ile Gly Gln Gly Ser Glu
820 825 830

Glu Leu Leu Pro Leu Lys Asp Arg Ile Tyr Gly Arg Thr Val Ala Glu
835 840 845

Asp Val Tyr Gln Pro Gly Asp Lys Ser Arg Leu Leu Ala Gln Ser Gly
850 855 860

Asp Val Leu Asn Ser Val Gln Ala Glu Ala Ile Asp Asp Ala Gly Ile
865 870 875 880

Glu Thr Ile Lys Ile Arg Ser Thr Leu Thr Cys Glu Ser Pro Arg Gly
885 890 895

Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Ala Asn Gly Arg Leu Ile
900 905 910

Gly Met Gly Glu Ala Val Gly Ile Ile Ala Ala Gln Ser Ile Gly Glu
915 920 925

Pro Gly Thr Gln Leu Thr Met Arg Thr Phe His Leu Gly Gly Ile Ala
930 935 940

Ala Thr Ser Ser Thr Pro Glu Ile Ile Thr Asn Ser Asp Gly Ile Leu
945 950 955 960

Val Tyr Met Asp Leu Arg Val Val Leu Gly Gln Glu Gly His Asn Leu
965 970 975

Val Leu Asn Lys Lys Gly Ala Leu His Val Val Gly Asp Glu Gly Arg
980 985 990

Thr Leu Asn Glu Tyr Lys Lys Leu Leu Ser Thr Lys Ser Ile Glu Ser
995 1000 1005

Leu Glu Val Phe Pro Val Glu Leu Gly Val Lys Ile Leu Val Ala
1010 1015 1020

Asp Gly Thr Pro Val Ser Gln Gly Gln Arg Ile Ala Glu Val Glu
1025 1030 1035

Leu His Asn Ile Pro Ile Ile Cys Asp Lys Pro Gly Phe Ile Lys
1040 1045 1050

Tyr Glu Asp Leu Val Glu Gly Ile Ser Thr Glu Lys Val Val Asn
1055 1060 1065

Lys Asn Thr Gly Leu Val Glu Leu Ile Val Lys Gln His Arg Gly
1070 1075 1080

Glu Leu His Pro Gln Ile Ala Ile Tyr Asp Asp Ala Asp Leu Ser
1085 1090 1095

Glu Leu Val Gly Thr Tyr Ala Ile Pro Ser Gly Ala Ile Ile Ser
1100 1105 1110

Val Glu Glu Gly Gln Arg Val Asp Pro Gly Met Leu Leu Ala Arg
1115 1120 1125

Leu Pro Arg Gly Ala Ile Lys Thr Lys Asp Ile Thr Gly Gly Leu
1130 1135 1140

Pro Arg Val Ala Glu Leu Val Glu Ala Arg Lys Pro Glu Asp Ala
1145 1150 1155

Ala Asp Ile Ala Lys Ile Asp Gly Val Val Asp Phe Lys Gly Ile
1160 1165 1170

Gln Lys Asn Lys Arg Ile Leu Val Val Cys Asp Glu Met Thr Gly
1175 1180 1185

Met Glu Glu Glu His Leu Ile Pro Leu Thr Lys His Leu Ile Val
1190 1195 1200

Gln Arg Gly Asp Ser Val Ile Lys Gly Gln Gln Leu Thr Asp Gly
1205 1210 1215

Leu Val Val Pro His Glu Ile Leu Glu Ile Cys Gly Val Arg Glu
1220 1225 1230

Leu Gln Lys Tyr Leu Val Asn Glu Val Gln Glu Val Tyr Arg Leu
1235 1240 1245

Gln Gly Val Asp Ile Asn Asp Lys His Ile Glu Ile Ile Val Arg
1250 1255 1260

Gln Met Leu Gln Lys Val Arg Ile Thr Asp Pro Gly Asp Thr Thr
1265 1270 1275

Leu Leu Phe Gly Glu Asp Val Asn Lys Lys Glu Phe Tyr Glu Glu
1280 1285 1290

Asn Arg Arg Thr Glu Glu Asp Gly Gly Lys Pro Ala Gln Ala Val
1295 1300 1305

Pro Val Leu Leu Gly Ile Thr Lys Ala Ser Leu Gly Thr Glu Ser
1310 1315 1320

Phe Ile Ser Ala Ala Ser Phe Gln Asp Thr Thr Arg Val Leu Thr
1325 1330 1335

Asp Ala Ala Cys Cys Ser Lys Thr Asp Tyr Leu Leu Gly Phe Lys
1340 1345 1350

Glu Asn Val Ile Met Gly His Met Ile Pro Gly Gly Thr Gly Phe
1355 1360 1365

Glu Thr His Lys Arg Ile Lys Gln Tyr Leu Glu Lys Glu Gln Glu
1370 1375 1380

Asp Leu Val Phe Asp Phe Val Ser Glu Thr Glu Cys Val Cys
1385 1390 1395

<210> 80

<211> 571

<212> PRT

<213> Chlamydia pneumoniae

<400> 80

Met Asp Thr Gln Ser Ser Ile Gly Asn Glu Glu Trp Arg Ile Ala Gly
1 5 10 15

Thr Ser Val Val Ser Gly Met Ala Leu Gly Lys Val Phe Phe Leu Gly
20 25 30

Thr Ser Pro Leu His Val Arg Glu Leu Thr Leu Pro Gln Glu Glu Val
35 40 45

Glu His Glu Ile His Arg Tyr Tyr Lys Ala Leu Asn Arg Ser Lys Ser
50 55 60

Asp Ile Val Ala Leu Glu Gln Glu Val Thr Gly Gln Gln Gly Leu Gln
65 70 75 80

Glu Val Ser Ser Ile Leu Gln Ala His Leu Glu Ile Met Lys Asp Pro
85 90 95

Leu Leu Thr Glu Glu Val Val Asn Thr Ile Arg Lys Asp Arg Lys Asn
100 105 110

Ala Glu Tyr Val Phe Ser Ser Val Met Gly Lys Ile Glu Glu Ser Leu
115 120 125

Thr Ala Val Arg Gly Met Pro Ser Val Val Asp Arg Val Gln Asp Ile
130 135 140

His Asp Ile Ser Asn Arg Val Ile Gly His Leu Cys Cys Gln His Lys
145 150 155 160

Ser Ser Leu Gly Glu Ser Asp Gln Asn Leu Ile Ile Phe Ser Glu Glu
165 170 175

Leu Thr Pro Ser Glu Val Ala Ser Ala Asn Ser Ala Tyr Ile Arg Gly
180 185 190

Phe Val Ser Leu Val Gly Ala Ala Thr Ser His Thr Ala Ile Val Ser
195 200 205

Arg Ala Lys Ser Ile Pro Tyr Leu Ala Asn Ile Ser Glu Glu Leu Trp
210 215 220

Asn Ile Ala Lys Arg Tyr Asn Gly Lys Leu Val Leu Ile Asp Gly Tyr
225 230 235 240

Arg Gly Glu Leu Ile Phe Asn Pro Lys Pro Ala Thr Leu Gln Ser Cys
245 250 255

Tyr Lys Lys Glu Leu Ser Val Val Ala His Thr Ser Gln Arg Leu Val
260 265 270

Arg Lys Ser Leu His Pro Ile Val Ser Ser His Ala Gly Ser Asp Lys
275 280 285

Asp Val Glu Asp Leu Leu Glu Asn Phe Pro Gln Thr Ser Ile Gly Leu
290 295 300

Phe Arg Ser Glu Phe Leu Ala Val Ile Leu Gly Arg Leu Pro Thr Leu
305 310 315 320

Arg Glu Gln Val Asp Leu Tyr Glu Lys Leu Ala Arg Phe Pro Gly Asp
325 330 335

Ser Pro Ser Val Leu Arg Leu Phe Asp Phe Gly Glu Asp Lys Pro Cys
340 345 350

Pro Gly Ile Lys Asn Lys Lys Glu Arg Ser Ile Arg Trp Leu Leu Asp
355 360 365

Tyr Ser Val Ile Leu Glu Asp Gln Leu Gln Ala Ile Ala Lys Ala Ser
370 375 380

Leu Gln Gly Ser Ile Lys Val Leu Ile Pro Gly Val Ser Asp Val Ser
385 390 395 400

Glu Ile Ile Glu Val Lys Lys Lys Trp Glu Thr Ile Gln Thr Arg Phe
405 410 415

Pro Lys Gly His Lys Val Ser Trp Gly Thr Met Ile Glu Phe Pro Ser
420 425 430

Ala Val Trp Met Ile Glu Glu Ile Leu Pro Glu Cys Asp Phe Leu Ser
435 440 445

Ile Gly Thr Asn Asp Leu Val Gln Tyr Thr Leu Gly Ile Ser Arg Glu
450 455 460

Ser Ala Leu Pro Lys His Leu Asn Val Thr Leu Pro Pro Ala Val Ile
465 470 475 480

Arg Met Ile His His Val Leu Gln Ala Ala Lys Gln Asn Gln Val Pro
485 490 495

Val Ser Ile Cys Gly Glu Ala Ala Gly Gln Leu Ser Leu Thr Pro Leu
500 505 510

Phe Ile Gly Leu Gly Val Gln Glu Leu Ser Val Ala Met Pro Val Ile
515 520 525

Asn Arg Leu Arg Asn His Ile Ala Leu Leu Glu Leu Asn Ser Cys Leu
530 535 540

Glu Ile Thr Glu Ala Leu Leu Gln Ala Lys Thr Cys Ser Glu Val Glu
545 550 555 560

Glu Leu Leu Asn Arg Asn Asn Lys Ile Thr Ser
565 570

<210> 81

<211> 460

<212> PRT

<213> Chlamydia pneumoniae

<400> 81

Met Arg Gln Glu Lys Asp Ser Leu Gly Ile Val Glu Val Pro Glu Asp
1 5 10 15

Lys Leu Tyr Gly Ala Gln Thr Met Arg Ser Arg Asn Phe Phe Ser Trp
20 25 30

Gly Pro Glu Leu Met Pro Tyr Glu Val Ile Arg Ala Leu Val Trp Ile
35 40 45

Lys Lys Cys Ala Ala Gln Ala Asn Gln Asp Leu Gly Phe Leu Asp Ser
50 55 60

Lys His Cys Asp Met Ile Val Ala Ala Ala Asp Glu Ile Leu Glu Gly
65 70 75 80

Gly Phe Glu Glu His Phe Pro Leu Lys Val Trp Gln Thr Gly Ser Gly
85 90 95

Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Asn Leu Ala Ile
100 105 110

Arg His His Gly Gly Val Leu Gly Ser Lys Asp Pro Ile His Pro Asn
115 120 125

Asp His Val Asn Lys Ser Gln Ser Ser Asn Asp Val Phe Pro Thr Ala
130 135 140

Met His Ile Ala Ala Val Ile Ser Leu Lys Asn Lys Leu Ile Pro Ala
145 150 155 160

Leu Asp His Met Ile Arg Val Leu Asp Ala Lys Val Glu Glu Phe Arg
165 170 175

His Asp Val Lys Ile Gly Arg Thr His Leu Met Asp Ala Val Pro Met
180 185 190

Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ser Ser Gln Leu Arg His Cys
195 200 205

Leu Glu Ser Ile Ala Phe Ser Leu Ala His Leu Tyr Glu Leu Ala Ile
210 215 220

Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Val Pro Glu Gly Phe Val
225 230 235 240

Glu Lys Ile Ile His Tyr Leu Arg Lys Glu Thr Asp Glu Pro Phe Ile
245 250 255

Pro Ala Ser Asn Tyr Phe Ser Ala Leu Ser Cys His Asp Ala Leu Val
260 265 270

Asp Ala His Gly Ser Leu Ala Thr Leu Ala Cys Ala Leu Thr Lys Ile
275 280 285

Ala Thr Asp Leu Ser Phe Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly
290 295 300

Glu Leu Phe Phe Pro Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly
305 310 315 320

Lys Val Asn Pro Thr Gln Cys Glu Ala Leu Gln Met Val Cys Ala Gln
325 330 335

Val Leu Gly Asn Asn Gln Thr Val Ile Ile Gly Gly Ser Arg Gly Asn
340 345 350

Phe Glu Leu Asn Val Met Lys Pro Val Ile Ile Tyr Asn Phe Leu Gln
355 360 365

Ser Val Asp Leu Leu Ser Glu Gly Met Arg Ala Phe Ser Glu Phe Phe
370 375 380

Val Lys Gly Leu Lys Val Asn Lys Ala Arg Leu Gln Asp Asn Ile Asn
385 390 395 400

Asn Ser Leu Met Leu Val Thr Ala Leu Ala Pro Val Leu Gly Tyr Asp
405 410 415

Lys Cys Ser Lys Ala Ala Leu Lys Ala Phe His Glu Ser Ile Ser Leu
420 425 430

Lys Glu Ala Cys Leu Ala Leu Gly Tyr Leu Ser Glu Lys Glu Phe Asp
435 440 445

Arg Leu Val Val Pro Glu Asn Met Val Gly Asn His
450 455 460

<210> 82

<211> 238

<212> PRT

<213> Chlamydia pneumoniae

<400> 82

Met Gly Leu Tyr Asp Arg Asp Tyr Ile Gln Asp Ser Arg Val Gln Gly
1 5 10 15

Thr Phe Ala Ser Arg Val Tyr Gly Trp Met Thr Ala Gly Leu Ile Val
20 25 30

Thr Ser Cys Val Ala Leu Gly Leu Tyr Phe Ser Gly Leu Tyr Arg Ser
35 40 45

Leu Phe Ser Phe Trp Trp Val Trp Cys Phe Ala Thr Leu Gly Val Ser
50 55 60

Phe Phe Ile Asn Ser Lys Ile Gln Thr Leu Ser Val Ser Ala Val Gly
65   70   75   80

Gly Leu Phe Leu Leu Tyr Ser Thr Leu Glu Gly Met Phe Phe Gly Thr
                85   90   95

Leu Leu Pro Val Tyr Ala Ala Gln Tyr Gly Gly Gly Val Ile Trp Ala
            100   105   110

Ala Phe Gly Ser Ala Ala Leu Val Phe Gly Leu Ala Ala Val Tyr Gly
        115   120   125

Ala Phe Thr Lys Ser Asp Leu Thr Lys Ile Ser Lys Ile Met Thr Phe
    130   135   140

Ala Leu Ile Gly Leu Leu Leu Val Thr Leu Val Phe Ala Val Val Ser
145   150   155   160

Met Phe Val Ser Met Pro Leu Ile Tyr Leu Leu Ile Cys Tyr Leu Gly
                165   170   175

Leu Val Ile Phe Val Gly Leu Thr Ala Ala Asp Ala Gln Ala Ile Arg
            180   185   190

Arg Ile Ser Ser Thr Ile Gly Asp Asn Asn Thr Leu Ser Tyr Lys Leu
        195   200   205

Ser Leu Met Phe Ala Leu Lys Met Tyr Cys Asn Val Ile Met Val Phe
    210   215   220

Trp Tyr Leu Leu Gln Ile Phe Ser Ser Ser Gly Asn Arg Asp
225   230   235

<210> 83

<211> 1609

<212> PRT

<213> Chlamydia pneumoniae

<400> 83

Met Val Ala Lys Lys Thr Val Arg Ser Tyr Arg Ser Ser Phe Ser His
1   5   10   15

Ser Val Ile Val Ala Ile Leu Ser Ala Gly Ile Ala Phe Glu Ala His
            20   25   30

Ser Leu His Ser Ser Glu Leu Asp Leu Gly Val Phe Asn Lys Gln Phe
        35   40   45

Glu Glu His Ser Ala His Val Glu Glu Ala Gln Thr Ser Val Leu Lys
50 55 60

Gly Ser Asp Pro Val Asn Pro Ser Gln Lys Glu Ser Glu Lys Val Leu
65 70 75 80

Tyr Thr Gln Val Pro Leu Thr Gln Gly Ser Ser Gly Glu Ser Leu Asp
85 90 95

Leu Ala Asp Ala Asn Phe Leu Glu His Phe Gln His Leu Phe Glu Glu
100 105 110

Thr Thr Val Phe Gly Ile Asp Gln Lys Leu Val Trp Ser Asp Leu Asp
115 120 125

Thr Arg Asn Phe Ser Gln Pro Thr Gln Glu Pro Asp Thr Ser Asn Ala
130 135 140

Val Ser Glu Lys Ile Ser Ser Asp Thr Lys Glu Asn Arg Lys Asp Leu
145 150 155 160

Glu Thr Glu Asp Pro Ser Lys Lys Ser Gly Leu Lys Glu Val Ser Ser
165 170 175

Asp Leu Pro Lys Ser Pro Glu Thr Ala Val Ala Ala Ile Ser Glu Asp
180 185 190

Leu Glu Ile Ser Glu Asn Ile Ser Ala Arg Asp Pro Leu Gln Gly Leu
195 200 205

Ala Phe Phe Tyr Lys Asn Thr Ser Ser Gln Ser Ile Ser Glu Lys Asp
210 215 220

Ser Ser Phe Gln Gly Ile Ile Phe Ser Gly Ser Gly Ala Asn Ser Gly
225 230 235 240

Leu Gly Phe Glu Asn Leu Lys Ala Pro Lys Ser Gly Ala Ala Val Tyr
245 250 255

Ser Asp Arg Asp Ile Val Phe Glu Asn Leu Val Lys Gly Leu Ser Phe
260 265 270

Ile Ser Cys Glu Ser Leu Glu Asp Gly Ser Ala Ala Gly Val Asn Ile
275 280 285

Val Val Thr His Cys Gly Asp Val Thr Leu Thr Asp Cys Ala Thr Gly
290 295 300

Leu Asp Leu Glu Ala Leu Arg Leu Val Lys Asp Phe Ser Arg Gly Gly
305 310 315 320

Ala Val Phe Thr Ala Arg Asn His Glu Val Gln Asn Asn Leu Ala Gly
325 330 335

Gly Ile Leu Ser Val Val Gly Asn Lys Gly Ala Ile Val Val Glu Lys
340 345 350

Asn Ser Ala Glu Lys Ser Asn Gly Gly Ala Phe Ala Cys Gly Ser Phe
355 360 365

Val Tyr Ser Asn Asn Glu Asn Thr Ala Leu Trp Lys Glu Asn Gln Ala
370 375 380

Leu Ser Gly Gly Ala Ile Ser Ser Ala Ser Asp Ile Asp Ile Gln Gly
385 390 395 400

Asn Cys Ser Ala Ile Glu Phe Ser Gly Asn Gln Ser Leu Ile Ala Leu
405 410 415

Gly Glu His Ile Gly Leu Thr Asp Phe Val Gly Gly Gly Ala Leu Ala
420 425 430

Ala Gln Gly Thr Leu Thr Leu Arg Asn Asn Ala Val Val Gln Cys Val
435 440 445

Lys Asn Thr Ser Lys Thr His Gly Gly Ala Ile Leu Ala Gly Thr Val
450 455 460

Asp Leu Asn Glu Thr Ile Ser Glu Val Ala Phe Lys Gln Asn Thr Ala
465 470 475 480

Ala Leu Thr Gly Gly Ala Leu Ser Ala Asn Asp Lys Val Ile Ile Ala
485 490 495

Asn Asn Phe Gly Glu Ile Leu Phe Glu Gln Asn Glu Val Arg Asn His
500 505 510

Gly Gly Ala Ile Tyr Cys Gly Cys Arg Ser Asn Pro Lys Leu Glu Gln
515 520 525

Lys Asp Ser Gly Glu Asn Ile Asn Ile Ile Gly Asn Ser Gly Ala Ile
530 535 540

Thr Phe Leu Lys Asn Lys Ala Ser Val Leu Glu Val Met Thr Gln Ala
545 550 555 560

Glu Asp Tyr Ala Gly Gly Gly Ala Leu Trp Gly His Asn Val Leu Leu
565 570 575

Asp Ser Asn Ser Gly Asn Ile Gln Phe Ile Gly Asn Ile Gly Gly Ser
580 585 590

Thr Phe Trp Ile Gly Glu Tyr Val Gly Gly Gly Ala Ile Leu Ser Thr
        595   600   605

Asp Arg Val Thr Ile Ser Asn Asn Ser Gly Asp Val Val Phe Lys Gly
    610   615   620

Asn Lys Gly Gln Cys Leu Ala Gln Lys Tyr Val Ala Pro Gln Glu Thr
625   630   635   640

Ala Pro Val Glu Ser Asp Ala Ser Ser Thr Asn Lys Asp Glu Lys Ser
                645   650   655

Leu Asn Ala Cys Ser His Gly Asp His Tyr Pro Pro Lys Thr Val Glu
            660   665   670

Glu Glu Val Pro Pro Ser Leu Leu Glu Glu His Pro Val Val Ser Ser
        675   680   685

Thr Asp Ile Arg Gly Gly Gly Ala Ile Leu Ala Gln His Ile Phe Ile
    690   695   700

Thr Asp Asn Thr Gly Asn Leu Arg Phe Ser Gly Asn Leu Gly Gly Gly
705   710   715   720

Glu Glu Ser Ser Thr Val Gly Asp Leu Ala Ile Val Gly Gly Gly Ala
                725   730   735

Leu Leu Ser Thr Asn Glu Val Asn Val Cys Ser Asn Gln Asn Val Val
            740   745   750

Phe Ser Asp Asn Val Thr Ser Asn Gly Cys Asp Ser Gly Gly Ala Ile
        755   760   765

Leu Ala Lys Lys Val Asp Ile Ser Ala Asn His Ser Val Glu Phe Val
    770   775   780

Ser Asn Gly Ser Gly Lys Phe Gly Gly Ala Val Cys Ala Leu Asn Glu
785   790   795   800

Ser Val Asn Ile Thr Asp Asn Gly Ser Ala Val Ser Phe Ser Lys Asn
                805   810   815

Arg Thr Arg Leu Gly Gly Ala Gly Val Ala Ala Pro Gln Gly Ser Val
            820   825   830

Thr Ile Cys Gly Asn Gln Gly Asn Ile Ala Phe Lys Glu Asn Phe Val
        835   840   845

Phe Gly Ser Glu Asn Gln Arg Ser Gly Gly Gly Ala Ile Ile Ala Asn
    850   855   860

Ser Ser Val Asn Ile Gln Asp Asn Ala Gly Asp Ile Leu Phe Val Ser
865 870 875 880

Asn Ser Thr Gly Ser Tyr Gly Gly Ala Ile Phe Val Gly Ser Leu Val
885 890 895

Ala Ser Glu Gly Ser Asn Pro Arg Thr Leu Thr Ile Thr Gly Asn Ser
900 905 910

Gly Asp Ile Leu Phe Ala Lys Asn Ser Thr Gln Thr Ala Ala Ser Leu
915 920 925

Ser Glu Lys Asp Ser Phe Gly Gly Gly Ala Ile Tyr Thr Gln Asn Leu
930 935 940

Lys Ile Val Lys Asn Ala Gly Asn Val Ser Phe Tyr Gly Asn Arg Ala
945 950 955 960

Pro Ser Gly Ala Gly Val Gln Ile Ala Asp Gly Gly Thr Val Cys Leu
965 970 975

Glu Ala Phe Gly Gly Asp Ile Leu Phe Glu Gly Asn Ile Asn Phe Asp
980 985 990

Gly Ser Phe Asn Ala Ile His Leu Cys Gly Asn Asp Ser Lys Ile Val
995 1000 1005

Glu Leu Ser Ala Val Gln Asp Lys Asn Ile Ile Phe Gln Asp Ala
1010 1015 1020

Ile Thr Tyr Glu Glu Asn Thr Ile Arg Gly Leu Pro Asp Lys Asp
1025 1030 1035

Val Ser Pro Leu Ser Ala Pro Ser Leu Ile Phe Asn Ser Lys Pro
1040 1045 1050

Gln Asp Asp Ser Ala Gln His His Glu Gly Thr Ile Arg Phe Ser
1055 1060 1065

Arg Gly Val Ser Lys Ile Pro Gln Ile Ala Ala Ile Gln Glu Gly
1070 1075 1080

Thr Leu Ala Leu Ser Gln Asn Ala Glu Leu Trp Leu Ala Gly Leu
1085 1090 1095

Lys Gln Glu Thr Gly Ser Ser Ile Val Leu Ser Ala Gly Ser Ile
1100 1105 1110

Leu Arg Ile Phe Asp Ser Gln Val Asp Ser Ser Ala Pro Leu Pro
1115 1120 1125

Thr Glu Asn Lys Glu Glu Thr Leu Val Ser Ala Gly Val Gln Ile
1130 1135 1140

Asn Met Ser Ser Pro Thr Pro Asn Lys Asp Lys Ala Val Asp Thr
1145 1150 1155

Pro Val Leu Ala Asp Ile Ile Ser Ile Thr Val Asp Leu Ser Ser
1160 1165 1170

Phe Val Pro Glu Gln Asp Gly Thr Leu Pro Leu Pro Pro Glu Ile
1175 1180 1185

Ile Ile Pro Lys Gly Thr Lys Leu His Ser Asn Ala Ile Asp Leu
1190 1195 1200

Lys Ile Ile Asp Pro Thr Asn Val Gly Tyr Glu Asn His Ala Leu
1205 1210 1215

Leu Ser Ser His Lys Asp Ile Pro Leu Ile Ser Leu Lys Thr Ala
1220 1225 1230

Glu Gly Met Thr Gly Thr Pro Thr Ala Asp Ala Ser Leu Ser Asn
1235 1240 1245

Ile Lys Ile Asp Val Ser Leu Pro Ser Ile Thr Pro Ala Thr Tyr
1250 1255 1260

Gly His Thr Gly Val Trp Ser Glu Ser Lys Met Glu Asp Gly Arg
1265 1270 1275

Leu Val Val Gly Trp Gln Pro Thr Gly Tyr Lys Leu Asn Pro Glu
1280 1285 1290

Lys Gln Gly Ala Leu Val Leu Asn Asn Leu Trp Ser His Tyr Thr
1295 1300 1305

Asp Leu Arg Ala Leu Lys Gln Glu Ile Phe Ala His His Thr Ile
1310 1315 1320

Ala Gln Arg Met Glu Leu Asp Phe Ser Thr Asn Val Trp Gly Ser
1325 1330 1335

Gly Leu Gly Val Val Glu Asp Cys Gln Asn Ile Gly Glu Phe Asp
1340 1345 1350

Gly Phe Lys His His Leu Thr Gly Tyr Ala Leu Gly Leu Asp Thr
1355 1360 1365

Gln Leu Val Glu Asp Phe Leu Ile Gly Gly Cys Phe Ser Gln Phe
1370 1375 1380

Phe Gly Lys Thr Glu Ser Gln Ser Tyr Lys Ala Lys Asn Asp Val
1385 1390 1395

Lys Ser Tyr Met Gly Ala Ala Tyr Ala Gly Ile Leu Ala Gly Pro
1400 1405 1410

Trp Leu Ile Lys Gly Ala Phe Val Tyr Gly Asn Ile Asn Asn Asp
1415 1420 1425

Leu Thr Thr Asp Tyr Gly Thr Leu Gly Ile Ser Thr Gly Ser Trp
1430 1435 1440

Ile Gly Lys Gly Phe Ile Ala Gly Thr Ser Ile Asp Tyr Arg Tyr
1445 1450 1455

Ile Val Asn Pro Arg Arg Phe Ile Ser Ala Ile Val Ser Thr Val
1460 1465 1470

Val Pro Phe Val Glu Ala Glu Tyr Val Arg Ile Asp Leu Pro Glu
1475 1480 1485

Ile Ser Glu Gln Gly Lys Glu Val Arg Thr Phe Gln Lys Thr Arg
1490 1495 1500

Phe Glu Asn Val Ala Ile Pro Phe Gly Phe Ala Leu Glu His Ala
1505 1510 1515

Tyr Ser Arg Gly Ser Arg Ala Glu Val Asn Ser Val Gln Leu Ala
1520 1525 1530

Tyr Val Phe Asp Val Tyr Arg Lys Gly Pro Val Ser Leu Ile Thr
1535 1540 1545

Leu Lys Asp Ala Ala Tyr Ser Trp Lys Ser Tyr Gly Val Asp Ile
1550 1555 1560

Pro Cys Lys Ala Trp Lys Ala Arg Leu Ser Asn Asn Thr Glu Trp
1565 1570 1575

Asn Ser Tyr Leu Ser Thr Tyr Leu Ala Phe Asn Tyr Glu Trp Arg
1580 1585 1590

Glu Asp Leu Ile Ala Tyr Asp Phe Asn Gly Gly Ile Arg Ile Ile
1595 1600 1605

Phe

<210> 84

<211> 253

<212> PRT

<213> Chlamydia pneumoniae

<400> 84

Met Leu Ile Lys Leu Trp Arg Ala Thr Tyr Glu Gly Met Tyr Thr Phe
1 5 10 15

Leu Val Gly Ala Leu Leu Lys Leu Arg Tyr Arg Met Gln Val Glu Gly
20 25 30

Trp Asp Thr Leu Asn Ile Asn Pro Lys Gln Gly Cys Leu Phe Leu Ala
35 40 45

Asn His Val Ala Glu Val Asp Pro Ile Ile Leu Glu Tyr Leu Phe Trp
50 55 60

Ser Arg Phe His Val Arg Pro Met Ala Val Glu Tyr Leu Phe His Ser
65 70 75 80

Arg Val Val Gln Trp Phe Leu Asn Ser Val Arg Ser Ile Pro Ile Pro
85 90 95

Gln Leu Val Pro Gly Lys Glu Ser Lys Arg Ser Leu Glu Arg Met Asn
100 105 110

Val Cys Tyr Glu Glu Ala Ser Arg Ala Leu Asn Arg Gly Glu Ser Leu
115 120 125

Leu Leu Tyr Pro Ser Gly Arg Leu Ser Arg Thr Gly Lys Glu Glu Ile
130 135 140

Val Asn Gln Tyr Ser Ala Tyr Val Leu Leu His Arg Val Met Glu Cys
145 150 155 160

Asn Val Val Leu Val Arg Val Ser Gly Leu Trp Gly Ser Ala Phe Ser
165 170 175

Arg Tyr Lys Gln Asn Ser Thr Pro Lys Leu Gly Pro Ala Phe Lys Glu
180 185 190

Ala Phe Arg Ala Leu Leu Arg Arg Gly Ile Phe Phe Met Pro Lys Arg
195 200 205

Phe Val Lys Ile Thr Leu Cys Gln Val Asp His Leu Phe Leu Lys Gln
210 215 220

Phe Pro Thr Lys Gln Asp Leu Asn Thr Phe Leu Ala Ser Trp Phe Asn
225 230 235 240

Gln Gly Asp Asp Asn Leu Pro Ile Glu Val Pro Tyr Ala
245 250

<210> 85

<211> 665

<212> PRT

<213> Chlamydia pneumoniae

<220>

<221> MISC_FEATURE

<222> (76)..(76)

<223> X may be any amino acid

<400> 85

Met Ile Asn Lys Glu Leu Asp Ile Gly Ile Leu Gly Lys Ile Ala Gly
1 5 10 15

Ala Ile Lys Gln Ile Ser Ile Glu Ser Ile Gln Lys Ala Ser Ser Gly
20 25 30

His Pro Gly Leu Pro Leu Gly Cys Ala Glu Leu Ala Ala Tyr Leu Tyr
35 40 45

Gly Tyr Val Leu Arg Gln Asn Pro Arg Asp Pro His Trp Ile Asn Arg
50 55 60

Asp Arg Phe Val Leu Ser Ala Gly His Gly Ser Xaa Leu Leu Tyr Ser
65 70 75 80

Cys Leu His Leu Ala Gly Phe Asp Val Ser Leu Glu Asp Leu Gln Glu
85 90 95

Phe Arg Gln Leu His Ser Arg Thr Pro Gly His Pro Glu Tyr Gly Glu
100 105 110

Thr Val Gly Val Glu Ala Thr Thr Gly Pro Leu Gly Gln Gly Leu Gly
115 120 125

Asn Ala Val Gly Met Ala Leu Ser Met Lys Met Leu Glu Ser Arg Phe
130 135 140

Asn Arg Pro Gly His Glu Ile Phe Asn Gly Lys Ile Tyr Cys Leu Ala
145 150 155 160

Gly Asp Gly Cys Phe Met Glu Gly Val Ser His Glu Val Cys Ser Phe
165 170 175

Ala Gly Ser Leu Asn Leu Asn Asn Leu Val Val Ile Tyr Asp Tyr Asn
180 185 190

Asn Val Val Leu Asp Gly Tyr Leu Asn Glu Ile Ser Val Glu Asp Thr
195 200 205

Lys Lys Arg Phe Glu Ala Tyr Gly Trp Asp Val Tyr Glu Ile Asp Gly
210 215 220

Tyr Asp Phe Thr His Ile His Glu Thr Phe Ser Ser Ile Lys Arg Gly
225 230 235 240

Gln Glu Arg Pro Val Leu Val Ile Ala His Thr Ile Ile Gly His Gly
245 250 255

Ser Pro Lys Glu Gly Thr Asn Lys Ala His Gly Ser Pro Leu Gly Val
260 265 270

Glu Gly Thr His Glu Thr Lys Gln Phe Trp His Leu Pro Glu Glu Lys
275 280 285

Phe Phe Val Pro Pro Ala Val Lys Asn Phe Phe Ala His Lys Ile Gln
290 295 300

Glu Asp Arg Lys Ala Gln Glu Gln Trp Leu Asp Glu Val Arg Val Trp
305 310 315 320

Ser Lys Gln Phe Pro Glu Leu His Glu Glu Phe Val Ala Leu Thr Ser
325 330 335

His Lys Leu Pro Lys Asn Leu Glu Ser Leu Val Gln Ser Val Glu Met
340 345 350

Pro Asp Ser Ile Ala Gly Arg Ala Ala Ser Asn Lys Leu Ile Gln Val
355 360 365

Leu Val Gln His Ile Pro Tyr Leu Ile Gly Gly Ser Ala Asp Leu Ser
370 375 380

Ser Ser Asp Gly Thr Trp Ile Ala Asn Glu Lys Val Ile His Thr Tyr
385 390 395 400

Asp Phe Ser Gly Arg Asn Ile Lys Tyr Gly Val Arg Glu Phe Gly Met
405 410 415

Ala Thr Ile Met Asn Gly Leu Ala Tyr Ser Gln Val Phe Arg Pro Phe
420 425 430

Gly Gly Thr Phe Leu Val Phe Ser Asp Tyr Met Arg Asn Ala Ile Arg
435 440 445

Leu Ala Ala Leu Ser Lys Leu Pro Val Ile Tyr Gln Phe Thr His Asp
450 455 460

Ser Ile Phe Val Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln
465 470 475 480

Leu Met Ser Leu Arg Ala Ile Pro Gly Leu Tyr Val Ile Arg Pro Ala
485 490 495

Asp Ala Asn Glu Val Arg Gly Ala Trp Ile Ala Gly Leu Lys His Thr
500 505 510

Gly Pro Thr Val Ile Val Leu Ser Arg Gln Ala Leu Pro Thr Leu Pro
515 520 525

Ala Ala His Arg Pro Phe Lys Asp Gly Val Gly Arg Gly Ala Tyr Ile
530 535 540

Val Leu Lys Glu Ser Gly Glu Lys Pro Asp Tyr Thr Leu Phe Ala Thr
545 550 555 560

Gly Ser Glu Val Ser Leu Ala Leu Ser Val Ala Lys Glu Leu Glu His
565 570 575

Leu Asp Lys Gln Val Arg Val Val Ser Phe Pro Cys Trp Glu Leu Phe
580 585 590

Glu Ala Gln Asp Val Asp Tyr Lys Gln Ser Ile Val Gly Gly Asp Leu
595 600 605

Gly Ile Arg Val Ser Ile Glu Ala Gly Ser Ala Leu Gly Trp Tyr Lys
610 615 620

Tyr Ile Gly Ser Glu Gly Leu Ala Ile Ala Met Asp Arg Phe Gly Tyr
625 630 635 640

Ser Gly Ala Ser Asp Asp Val Ser Glu Glu Cys Gly Phe Thr Thr Glu
645 650 655

Gln Ile Leu Gln Arg Ile Leu Ser Gln
660 665

<210> 86

<211> 401

<212> PRT

<213> Chlamydia pneumoniae

<400> 86

Met Ser Thr Met Gln Asn Cys Pro His Phe Gly Val Cys Gly Gly Cys
1   5   10   15

Ser Phe Pro Gln Ser Asn Tyr Ser Asp Ser Leu Lys Lys Lys Glu Glu
            20   25   30

Leu Leu His Gln Leu Phe Ala Pro Leu Val Pro Ser Asp Met Ile Ala
        35   40   45

Pro Ile Ile Pro Cys Ser Pro Ser Leu Arg Gly Arg Asn Lys Met Glu
    50   55   60

Phe Ser Phe Phe Gln Thr Tyr Glu Gly Glu Lys Ser Leu Gly Phe Ile
65   70   75   80

Ser Ser Thr Lys Pro Lys Lys Gly Ile Pro Val Thr Thr Cys Leu Leu
                85   90   95

Ile His Glu Gln Thr Met Asp Ile Leu Lys Leu Thr Arg Glu Trp Trp
            100   105   110

Asp Lys His Pro Glu Leu Met Ala Tyr Phe Pro Pro Lys Asn Lys Gly
        115   120   125

Ser Leu Cys Thr Leu Thr Val Arg Thr Gly Ser Pro Gln Gln Asn Phe
    130   135   140

Met Val Ile Leu Thr Thr Ser Gly Thr Pro Glu Tyr Arg Val Asn Glu
145   150   155   160

Ala Cys Ile Asp Glu Trp Lys Glu Ile Leu Leu Ser Ser Ser Leu Asn
                165   170   175

Ile Ala Ser Ile Tyr Trp Glu Glu Lys Val Ala Ala Arg Gly Ile Ser
            180   185   190

Thr Tyr Tyr Glu Thr Lys Leu Leu Tyr Gly Ala Pro Ser Ile Gln Gln
        195   200   205

Lys Leu Ser Leu Pro Ser Asp Gly Asn Ser Ala Ser Phe Ser Leu Arg
    210   215   220

Pro Arg Ser Phe Phe Gln Pro Gln Ile Thr Gln Ala Ala Lys Ile Ile
225   230   235   240

Glu Thr Ala Lys Glu Phe Ile Asn Pro Glu Gly Ser Glu Thr Leu Leu
                245   250   255

Asp Leu Tyr Cys Gly Ala Gly Thr Ile Gly Ile Met Leu Ser Pro Tyr
            260   265   270

Val Lys Asn Val Ile Gly Val Glu Ile Ile Pro Asp Ala Val Ala Ser
        275   280   285

Ala Gln Glu Asn Ile Lys Ala Asn Asn Lys Glu Asp Cys Val Glu Val
    290   295   300

Tyr Leu Glu Asp Ala Lys Ala Phe Cys Lys Arg Asn Glu Asn Cys Lys
305   310   315   320

Ala Pro Asp Val Ile Ile Ile Asp Pro Pro Arg Cys Gly Met Gln Ser
                325   330   335

Lys Val Leu Lys Tyr Ile Leu Arg Ile Gly Ser Pro Lys Ile Val Tyr
            340   345   350

Ile Ser Cys Asn Pro Lys Thr Gln Phe Gln Glu Cys Ala Asp Leu Ile
        355   360   365

Ser Gly Gly Tyr Arg Ile Lys Lys Met Gln Pro Ile Asp Gln Phe Pro
    370   375   380

Tyr Ser Thr His Leu Glu Asn Ile Ile Leu Leu Glu Arg Glu Ile Asp
385   390   395   400

Leu

<210> 87

<211> 444

<212> PRT

<213> Chlamydia pneumoniae

<400> 87

Met Thr Ser Gly Val Ser Gly Ser Ser Ser Gln Asp Pro Thr Leu Ala
1   5   10   15

Ala Gln Leu Ala Gln Ser Ser Gln Lys Ala Gly Asn Ala Gln Ser Gly
            20   25   30

His Asp Thr Lys Asn Val Thr Lys Gln Gly Ala Gln Ala Glu Val Ala
        35   40   45

Ala Gly Gly Phe Glu Asp Leu Ile Gln Asp Ala Ser Ala Gln Ser Thr
    50   55   60

Gly Lys Lys Glu Ala Thr Ser Ser Thr Thr Lys Ser Ser Lys Gly Glu
65   70   75   80

Lys Ser Glu Lys Ser Gly Lys Ser Lys Ser Ser Thr Ser Val Ala Ser
85 90 95

Ala Ser Glu Thr Ala Thr Ala Gln Ala Val Gln Gly Pro Lys Gly Leu
100 105 110

Arg Gln Asn Asn Tyr Asp Ser Pro Ser Leu Pro Thr Pro Glu Ala Gln
115 120 125

Thr Ile Asn Gly Ile Val Leu Lys Lys Gly Met Gly Thr Leu Ala Leu
130 135 140

Leu Gly Leu Val Met Thr Leu Met Ala Asn Ala Ala Gly Glu Ser Trp
145 150 155 160

Lys Ala Ser Phe Gln Ser Gln Asn Gln Ala Ile Arg Ser Gln Val Glu
165 170 175

Ser Ala Pro Ala Ile Gly Glu Ala Ile Lys Arg Gln Ala Asn His Gln
180 185 190

Ala Ser Ala Thr Glu Ala Gln Ala Lys Gln Ser Leu Ile Ser Gly Ile
195 200 205

Val Asn Ile Val Gly Phe Thr Val Ser Val Gly Ala Gly Ile Phe Ser
210 215 220

Ala Ala Lys Gly Ala Thr Ser Ala Leu Lys Ser Ala Ser Phe Ala Lys
225 230 235 240

Glu Thr Gly Ala Ser Ala Ala Gly Gly Ala Ala Ser Lys Ala Leu Thr
245 250 255

Ser Ala Ser Ser Ser Val Gln Gln Thr Met Ala Ser Thr Ala Lys Ala
260 265 270

Ala Thr Thr Ala Ala Ser Ser Ala Gly Ser Ala Ala Thr Lys Ala Ala
275 280 285

Ala Asn Leu Thr Asp Asp Met Ala Ala Ala Ala Ser Lys Met Ala Ser
290 295 300

Asp Gly Ala Ser Lys Ala Ser Gly Gly Leu Phe Gly Glu Val Leu Asn
305 310 315 320

Lys Pro Asn Trp Ser Glu Lys Val Ser Arg Gly Met Asn Val Val Lys
325 330 335

Thr Gln Gly Ala Arg Val Ala Ser Phe Ala Gly Asn Ala Leu Ser Ser
340 345 350

Ser Met Gln Met Ser Gln Leu Met His Gly Leu Thr Ala Ala Val Glu
355 360 365

Gly Leu Ser Ala Gly Gln Thr Gly Ile Glu Val Ala His His Gln Arg
370 375 380

Leu Ala Gly Gln Ala Glu Ala Gln Ala Glu Val Leu Lys Gln Met Ser
385 390 395 400

Ser Val Tyr Gly Gln Gln Ala Gly Gln Ala Gly Gln Leu Gln Glu Gln
405 410 415

Ala Met Gln Ser Phe Asn Thr Ala Leu Gln Thr Leu Gln Asn Ile Ala
420 425 430

Asp Ser Gln Thr Gln Thr Thr Ser Ala Ile Phe Asn
435 440

<210> 88

<211> 674

<212> PRT

<213> Chlamydia pneumoniae

<400> 88

Met Ser Ile Val Arg Asn Ser Ala Leu Pro Leu Pro Cys Leu Ser Arg
1 5 10 15

Ser Glu Thr Phe Lys Lys Val Arg Ser His Met Lys Phe Met Lys Val
20 25 30

Leu Thr Pro Trp Ile Tyr Arg Lys Asp Leu Trp Val Thr Ala Phe Leu
35 40 45

Leu Thr Ala Ile Pro Gly Ser Phe Ala His Thr Leu Val Asp Ile Ala
50 55 60

Gly Glu Pro Arg His Ala Ala Gln Ala Thr Gly Val Ser Gly Asp Gly
65 70 75 80

Lys Ile Val Ile Gly Met Lys Val Pro Asp Asp Pro Phe Ala Ile Thr
85 90 95

Val Gly Phe Gln Tyr Ile Asp Gly His Leu Gln Pro Leu Glu Ala Val
100 105 110

Arg Pro Gln Cys Ser Val Tyr Pro Asn Gly Ile Thr Pro Asp Gly Thr
115 120 125

Val Ile Val Gly Thr Asn Tyr Ala Ile Gly Met Gly Ser Val Ala Val
130 135 140

Lys Trp Val Asn Gly Lys Val Ser Glu Leu Pro Met Leu Pro Asp Thr
145 150 155 160

Leu Asp Ser Val Ala Ser Ala Val Ser Ala Asp Gly Arg Val Ile Gly
165 170 175

Gly Asn Arg Asn Ile Asn Leu Gly Ala Ser Val Ala Val Lys Trp Glu
180 185 190

Asp Asp Val Ile Thr Gln Leu Pro Ser Leu Pro Asp Ala Met Asn Ala
195 200 205

Cys Val Asn Gly Ile Ser Ser Asp Gly Ser Ile Ile Val Gly Thr Met
210 215 220

Val Asp Val Ser Trp Arg Asn Thr Ala Val Gln Trp Ile Gly Asp Gln
225 230 235 240

Leu Ser Val Ile Gly Thr Leu Gly Gly Thr Thr Ser Val Ala Ser Ala
245 250 255

Ile Ser Thr Asp Gly Thr Val Ile Val Gly Gly Ser Glu Asn Ala Asp
260 265 270

Ser Gln Thr His Ala Tyr Ala Tyr Lys Asn Gly Val Met Ser Asp Ile
275 280 285

Gly Thr Leu Gly Gly Phe Tyr Ser Leu Ala His Ala Val Ser Ser Asp
290 295 300

Gly Ser Val Ile Val Gly Val Ser Thr Asn Ser Glu His Arg Tyr His
305 310 315 320

Ala Phe Gln Tyr Ala Asp Gly Gln Met Val Asp Leu Gly Thr Leu Gly
325 330 335

Gly Pro Glu Ser Tyr Ala Gln Gly Val Ser Gly Asp Gly Lys Val Ile
340 345 350

Val Gly Arg Ala Gln Val Pro Ser Gly Asp Trp His Ala Phe Leu Cys
355 360 365

Pro Phe Gln Ala Pro Ser Pro Ala Pro Val His Gly Gly Ser Thr Val
370 375 380

Val Thr Ser Gln Asn Pro Arg Gly Met Val Asp Ile Asn Ala Thr Tyr
385 390 395 400

Ser Ser Leu Lys Asn Ser Gln Gln Gln Leu Gln Arg Leu Leu Ile Gln
405 410 415

His Ser Ala Lys Val Glu Ser Val Ser Ser Gly Ala Pro Ser Phe Thr
420 425 430

Ser Val Lys Gly Ala Ile Ser Lys Gln Ser Pro Ala Val Gln Asn Asp
435 440 445

Val Gln Lys Gly Thr Phe Leu Ser Tyr Arg Ser Gln Val His Gly Asn
450 455 460

Val Gln Asn Gln Gln Leu Leu Thr Gly Ala Phe Met Asp Trp Lys Leu
465 470 475 480

Ala Ser Ala Pro Lys Cys Gly Phe Lys Val Ala Leu His Tyr Gly Ser
485 490 495

Gln Asp Ala Leu Val Glu Arg Ala Ala Leu Pro Tyr Thr Glu Gln Gly
500 505 510

Leu Gly Ser Ser Val Leu Ser Gly Phe Gly Gly Gln Val Gln Gly Arg
515 520 525

Tyr Asp Phe Asn Leu Gly Glu Thr Val Val Leu Gln Pro Phe Met Gly
530 535 540

Ile Gln Val Leu His Leu Ser Arg Glu Gly Tyr Ser Glu Lys Asn Val
545 550 555 560

Arg Phe Pro Val Ser Tyr Asp Ser Val Ala Tyr Ser Ala Ala Thr Ser
565 570 575

Phe Met Gly Ala His Val Phe Ala Ser Leu Ser Pro Lys Met Ser Thr
580 585 590

Ala Ala Thr Leu Gly Val Glu Arg Asp Leu Asn Ser His Ile Asp Glu
595 600 605

Phe Lys Gly Ser Val Ser Ala Met Gly Asn Phe Val Leu Glu Asn Ser
610 615 620

Thr Val Ser Val Leu Arg Pro Phe Ala Ser Leu Ala Met Tyr Tyr Asp
625 630 635 640

Val Arg Gln Gln Gln Leu Val Thr Leu Ser Val Val Met Asn Gln Gln
645 650 655

Pro Leu Thr Gly Thr Leu Ser Leu Val Ser Gln Ser Ser Tyr Asn Leu
660 665 670

Ser Phe

<210> 89

<211> 609

<212> PRT

<213> Chlamydia pneumoniae

<400> 89

Met Phe Arg Cys Ile Leu Phe Gly Ile Phe Leu Leu Thr Cys Phe Ser
1 5 10 15

Ser Gly Gly Val Leu Tyr Tyr Leu Phe Cys Ser His Asp Phe Ser Ile
20 25 30

Gly Pro Lys Glu Lys Ser Arg Ser Val Trp Ile Glu Glu Glu Lys Glu
35 40 45

Phe Thr Asp Ser Val Leu His His Leu Pro Ser Gln His Gln His Leu
50 55 60

His Ile Leu Cys Phe Gln Gly Phe Leu Leu Gln Lys Gln Gln Lys Phe
65 70 75 80

Ser Gln Ala Glu Lys Ile Phe Ser Lys Val Tyr Asp Glu Ala Gln Asp
85 90 95

Gly Pro Phe Leu Phe Lys Glu Glu Ile Leu Gly Ser Arg Leu Ile Asn
100 105 110

Ser Phe Phe Leu Glu Lys Thr Asp Val Met Glu Thr Ile Leu Cys Leu
115 120 125

Leu Asn Gln Arg Cys Pro Asn Ser Pro Tyr Tyr His Leu Phe Lys Ala
130 135 140

Leu Val Cys Tyr Lys Gln Lys Leu Tyr Arg Glu Val Ile Glu Gln Leu
145 150 155 160

Ala Tyr Trp Gln Glu Glu Lys Thr Arg Ala Leu Ala Pro Leu Leu Asn
165 170 175

Ile Ser Ile Glu Gln Leu Leu Thr Asp Phe Leu Leu Asp Tyr Ile Ser
180 185 190

Ala His Ser Leu Ile Glu Gln Lys Met Phe Pro Glu Gly Arg Val Ile
195 200 205

Leu Asn Arg Asn Ile Asn Arg Leu Leu Lys His Glu Cys Glu Trp Asn
210 215 220

Ala Lys Thr Tyr Asp Arg Ile Ala Ile Leu Leu Ser Arg Ser Tyr Phe
225 230 235 240

Leu Glu Leu Val Glu Ser Lys Ser Ala Asp Ile Tyr Phe Asp Tyr Tyr
245 250 255

Glu Met Val Leu Phe Tyr Leu Lys Lys Ile Tyr Ile Leu Glu Gln Cys
260 265 270

Pro Tyr Ala Glu Leu Leu Pro Glu Glu Glu Leu Val Ser Leu Ile Met
275 280 285

Glu His Val Phe Ile Leu Pro Lys Asp Lys Leu Tyr Pro Leu Ile Gln
290 295 300

Leu Leu Glu Met Trp Gln Lys His Tyr Val His Pro Asn Ser Ser Leu
305 310 315 320

Val Val Gln Ile Leu Val Asp Arg Phe Ser Thr His Met Glu Gly Ala
325 330 335

Ile Arg Phe Cys Glu Ala Leu Val Ser Phe Ser Gly Leu Glu Glu Leu
340 345 350

His Gln Gln Ile Ile Thr Thr Phe Glu Glu Leu Leu Ser Asn Lys Val
355 360 365

Gln Gln Ile Lys Thr Glu Glu Ala Lys Gln Cys Val Ala Leu Leu His
370 375 380

Ile Leu Asp Pro Ser Ile Ser Ile Ser Glu Lys Leu Ala Leu Ser Ser
385 390 395 400

Asp Thr Leu Gln Asn Ile Val Ser Gly Asp Asp Glu Gln His Thr Lys
405 410 415

Leu Arg Asn Tyr Leu Asp Leu Trp Glu Ala Ile Gln Ser Tyr Asp Ile
420 425 430

Asp Arg Gln Gln Leu Val His His Leu Val Tyr Gly Ala Lys Asp Leu
435 440 445

Trp Lys Lys Gly Gly Asn Asp Glu Lys Ala Leu Asn Leu Leu Gln Leu
450 455 460

Val Leu Arg Phe Thr Ser Tyr Asp Ile Glu Cys Glu Ser Val Val Phe
465 470 475 480

Leu Phe Ile Lys Gln Ala Tyr Lys Gln Ala Leu Ser Ser His Ala Ile
485 490 495

Ala Arg Leu Leu Lys Leu Glu Lys Phe Ile Ser Glu Ala Asn Ile Pro
500 505 510

Ser Ile Val Ile Ser Glu Ala Glu Lys Ala Asn Phe Leu Ala Asp Ala
515 520 525

Glu Tyr Leu Phe Ala His Glu Asp Tyr Asp Lys Cys Tyr Leu Tyr Ser
530 535 540

Met Trp Leu Thr Lys Val Ala Pro Ser Pro Gln Ser Tyr Arg Leu Ala
545 550 555 560

Gly Leu Cys Leu Met Glu Asn Lys Arg Tyr Asp Glu Ala Leu Glu Phe
565 570 575

Leu Cys Met Leu Ser Pro Asn Asn Ser Ile Asn Asp Tyr Lys Thr Gln
580 585 590

Lys Ala Leu Ala Phe Cys Gln Lys His Gln Ser Lys Asp Arg Ala Ala
595 600 605

Ser

<210> 90

<211> 531

<212> PRT

<213> Chlamydia pneumoniae

<400> 90

Met Leu Gly Lys Glu Glu Glu Phe Thr Cys Lys Gln Lys Gln Cys Leu
1 5 10 15

Ser His Phe Val Thr Asn Leu Thr Ser Asp Val Phe Ala Leu Lys Asn
20 25 30

Leu Pro Glu Val Val Lys Gly Ala Leu Phe Ser Lys Tyr Ser Arg Ser
35 40 45

Val Leu Gly Leu Arg Ala Leu Leu Leu Lys Glu Phe Leu Ser Asn Glu
50 55 60

Glu Asp Gly Asp Val Cys Asp Glu Ala Tyr Asp Phe Glu Thr Asp Val
65 70 75 80

Gln Lys Ala Ala Asp Phe Tyr Gln Arg Val Leu Asp Asn Phe Gly Asp
85 90 95

Asp Ser Val Gly Glu Leu Gly Gly Ala His Leu Ala Met Glu Asn Val
100 105 110

Ser Ile Leu Ala Ala Lys Val Leu Glu Asp Ala Arg Ile Gly Gly Ser
115 120 125

Pro Leu Glu Lys Ser Thr Arg Tyr Val Tyr Phe Asp Gln Lys Val Arg
130 135 140

Gly Glu Tyr Leu Tyr Tyr Arg Asp Pro Ile Leu Met Thr Ser Ala Phe
145 150 155 160

Lys Asp Met Phe Leu Gly Thr Cys Asp Phe Leu Phe Asp Thr Tyr Ser
165 170 175

Ala Leu Ile Pro Gln Val Arg Ala Tyr Phe Glu Lys Leu Tyr Pro Lys
180 185 190

Asp Ser Lys Thr Pro Ala Ser Ala Tyr Ala Thr Ser Leu Arg Ala Lys
195 200 205

Val Leu Asp Cys Ile Arg Gly Leu Leu Pro Ala Ala Thr Leu Thr Asn
210 215 220

Leu Gly Phe Phe Gly Asn Gly Arg Phe Trp Gln Asn Leu Ile His Lys
225 230 235 240

Leu Gln Gly His Asn Leu Ala Glu Leu Arg Arg Leu Gly Asp Glu Ser
245 250 255

Leu Thr Glu Leu Met Lys Val Ile Pro Ser Phe Val Ser Arg Ala Glu
260 265 270

Pro His His His His His Gln Ala Met Met Gln Tyr Arg Arg Ala Leu
275 280 285

Lys Glu Gln Leu Lys Gly Leu Ala Glu Gln Ala Thr Phe Ser Glu Glu
290 295 300

Met Ser Ser Ser Pro Ser Val Gln Leu Val Tyr Gly Asp Pro Asp Gly
305 310 315 320

Ile Tyr Lys Val Ala Ala Gly Phe Leu Phe Pro Tyr Ser Asn Arg Ser
325 330 335

Leu Thr Asp Leu Ile Asp Tyr Cys Lys Lys Met Pro His Glu Asp Leu
340 345 350

Val Gln Ile Leu Glu Ser Ser Val Ser Ala Arg Glu Asn Arg Arg His
355 360 365

Lys Ser Pro Arg Gly Leu Glu Cys Val Glu Phe Gly Phe Asp Ile Leu
370 375 380

Ala Asp Phe Gly Ala Tyr Arg Asp Leu Gln Arg His Arg Thr Leu Thr
385 390 395 400

Gln Glu Arg Gln Leu Leu Ser Thr His His Gly Tyr Asn Phe Pro Val
405 410 415

Glu Leu Leu Asp Thr Pro Met Glu Lys Ser Tyr Arg Glu Ala Met Glu
420 425 430

Arg Ala Asn Glu Thr Tyr Asn Glu Ile Val Gln Glu Phe Pro Glu Glu
435 440 445

Ala Gln Tyr Met Val Pro Met Ala Tyr Asn Ile Arg Trp Phe Phe His
450 455 460

Val Asn Ala Arg Ala Leu Gln Trp Ile Cys Glu Leu Arg Ser Gln Pro
465 470 475 480

Gln Gly His Gln Asn Tyr Arg Thr Ile Ala Thr Gly Leu Val Arg Glu
485 490 495

Val Val Lys Phe Asn Pro Met Tyr Glu Leu Phe Phe Lys Phe Val Asp
500 505 510

Tyr Ser Asp Ile Asp Leu Gly Arg Leu Asn Gln Glu Met Arg Lys Glu
515 520 525

Pro Thr Thr
530

<210> 91

<211> 31

<212> PRT

<213> Chlamydia pneumoniae

<400> 91

Arg Val Met Lys Ala Val Val Ser His Lys Ser Arg Thr Ser Ser Ile
1 5 10 15

His Arg Gln Tyr Ser Ser Tyr Ser Leu Phe Tyr Ser Ile Leu Lys
20 25 30

<210> 92

<211> 33

<212> PRT

<213> Chlamydia pneumoniae

<400> 92

Asp Gly Val Asn Phe Gly Asn Leu Phe Gln Pro Cys Pro Tyr Cys Arg
1 5 10 15

Gly Lys Tyr Pro Ser Pro Thr Cys Thr Ser Thr Leu Ser Pro Ser Ser
20 25 30

Ser

<210> 93

<211> 30

<212> PRT

<213> Chlamydia pneumoniae

<400> 93

Gly Leu Arg Arg Phe Cys Lys Arg Tyr Ser Ile Val Val Ser Glu Ser
1 5 10 15

Gly Glu Pro Phe Cys Leu Leu Lys Lys Lys Lys Ile Phe Leu
20 25 30

<210> 94

<211> 101

<212> PRT

<213> Chlamydia pneumoniae

<400> 94

Asn Phe Pro Ile Cys Asp Arg Ser Ser Arg Phe Arg Gly Asp Cys Arg
1 5 10 15

Asp Glu Asp Leu Cys Gly Arg Asn Arg Tyr Glu Ala Phe Pro Asp Asp
20 25 30

Lys Thr Glu Gly His Leu Cys Ser Cys Asp Thr Leu Ala Leu Ser Lys
35 40 45

Tyr Cys Cys Leu His Ser His Gly Ile Trp Trp Ile Asp Ser His Ala
50 55 60

Ser Ser Pro Cys Cys Phe Cys Arg Ile Gly Gly Cys Phe Cys Asn Thr
65 70 75 80

Pro Tyr Gly Phe Leu Arg Ile Phe Leu Arg Arg Leu Pro Thr Glu Ser
85 90 95

Lys Ile Glu Tyr Gln
100

<210> 95

<211> 21

<212> PRT

<213> Chlamydia pneumoniae

<400> 95

Phe Leu Pro Val Leu Pro Gly Leu Leu Leu Gly Pro Pro Leu Pro Gln
1 5 10 15

Met Ser Phe Arg Leu
20

<210> 96

<211> 63

<212> PRT

<213> Chlamydia pneumoniae

<400> 96

Phe Phe Ile Lys Tyr Ser Leu Ser Asn Gly Tyr Gly Ile Gln Lys Tyr
1 5 10 15

Leu Gln Thr Arg Leu Ser Ala Ile Pro Glu Trp His Phe Ser Gly Thr
20 25 30

Asn Thr Ser Ser Lys Ile Lys Lys Leu Cys Glu Glu Leu Ser Gln Asn
35 40 45

Cys Ser Tyr His Arg Ser Thr Gly Ile Leu Gly Leu Arg Ser Ser
50 55 60

<210> 97

<211> 69

<212> PRT

<213> Chlamydia pneumoniae

<400> 97

Cys Ser Tyr Ser Val Tyr Ser Leu Trp Ser Leu Leu Gln Leu Leu Met
1 5 10 15

Leu Met Lys Ser Glu Lys Lys Lys Ser Lys Phe Phe Asn Val Ser His
20 25 30

His Phe Gln Lys Val Leu Arg Leu Ser Glu Asp Asn Met Val Gln Glu
35 40 45

Arg Phe Lys Glu Ser Arg Ser Leu Ala Ile Val Lys Lys Arg Met Leu
50 55 60

Thr Lys Ile Pro Glu
65

<210> 98

<211> 12

<212> PRT

<213> Chlamydia pneumoniae

<400> 98

Ala Gln Ala Phe Gly Ser Leu Leu Leu Arg Met Leu
1 5 10

<210> 99

<211> 25

<212> PRT

<213> Chlamydia pneumoniae

<400> 99

Glu Leu Leu Ile Ser Tyr Gln Arg Lys Thr Ser Ser Ala Ile Gly Lys
1 5 10 15

Lys Asn Phe Thr Thr Ser Ser Gln Cys
20 25

<210> 100

<211> 32

<212> PRT

<213> Chlamydia pneumoniae

<400> 100

Glu Gly Arg Glu Asp Leu Pro Ser Ala Leu Arg Lys Gly Ser Pro Thr
1 5 10 15

Ser Gly Asn Ser Asn Phe Arg Ser Ala Ala Tyr Cys Gly Ser Cys Cys
20 25 30

<210> 101

<211> 33

<212> PRT

<213> Chlamydia pneumoniae

<400> 101

Arg Leu Arg Ser Thr Thr Asn Thr Ser Gln Ser Ser Pro Gln Trp Asp
1 5 10 15

Cys Thr His Pro Ile Tyr Leu Cys Asp Val Pro His Gly Ser Gly Tyr
20 25 30

Val

<210> 102

<211> 20

<212> PRT

<213> Chlamydia pneumoniae

<400> 102

Ala Pro Gln Ala Arg Gly Asp Thr Lys Ile Arg Gly Tyr Arg Asn Arg
1 5 10 15

Thr Arg Ala Cys
20

<210> 103

<211> 113

<212> PRT

<213> Chlamydia pneumoniae

<400> 103

Gly Arg Leu Leu Lys Gln Cys Met Leu Ser Ser Leu Arg Lys Trp Leu
1   5   10   15

Ala Ile Leu Gln Leu Phe Leu Ile Ala Gln Glu Lys Leu Arg Thr Leu
            20   25   30

Arg Leu Gln Ile Leu Leu Leu Pro Ser Thr Leu Val Lys Ser Lys Gln
        35   40   45

Ala Leu Tyr His Val Leu Ser Val Leu Gln Asn Thr Ile Asp Ser Trp
    50   55   60

Lys Leu Lys Lys Ser Leu Asp Pro Lys Gln Phe Ser Gln Ile Leu Met
65   70   75   80

Tyr Phe Leu Thr Arg Ile Leu Arg Asn Arg Gly Ile Phe Ser Ile Ser
                85   90   95

Ile Leu Ser Pro Asn Gln Glu Tyr Ile Ala Asp Leu Trp Ala Leu Ser
            100   105   110

Phe

<210> 104

<211> 20

<212> PRT

<213> Chlamydia pneumoniae

<400> 104

Ser Thr Asn Pro Thr Val Ala Leu Ala Ser Ile Phe Asp Ala Lys Thr
1   5   10   15

Thr Lys Cys Pro
            20

<210> 105

<211> 55

<212> PRT

<213> Chlamydia pneumoniae

<400> 105

Thr Asp Ile Leu Val Lys Phe Ile Lys Asn Ile Phe Pro Pro Leu Trp
1   5   10   15

Arg Gly Asn Val Val Pro Arg Ser Lys Asn Met Thr Ser Ile Tyr Thr
            20   25   30

His Ala Asn Gly Asn Leu Ile Phe Gln Ile Leu Asn Glu Val Thr Gln
        35   40   45

Phe Phe Lys Val Thr Pro Asn
    50   55

<210> 106

<211> 26

<212> PRT

<213> Chlamydia pneumoniae

<400> 106

Ser Ser Arg Cys Thr Gln Arg Glu Ile Ala Gly Arg Arg Thr Val Asn
1   5   10   15

Thr Pro Lys Pro Lys Arg Cys Met Gly Ser
            20   25

<210> 107

<211> 128

<212> PRT

<213> Chlamydia pneumoniae

<400> 107

Ile Asp Ala Thr Gln Ile Asn Leu Asn Ala Ser Gln Val Asp Ile His
1   5   10   15

Ile Arg Asn His Ser Ser Ser Tyr Trp Ser Ala Arg Thr Cys Met Arg
            20   25   30

Arg Arg Val Ser Pro Ser Thr Trp Ser Phe Ile Tyr Lys Gly Glu Val
        35   40   45

Trp Ser Trp Gly Arg Phe Pro Val Asn Ala Phe Gln Ala Pro Asn Ile
    50   55   60

Ile Pro Asn Arg Thr Cys Phe Tyr Phe Cys Ser Thr Thr Pro Cys Arg
65   70   75   80

Gly Cys Ile Ser Thr Thr Arg Phe Phe Ser Ile Pro Arg Thr Val Asp
85 90 95

Tyr Ser Ser Phe Lys Phe His Ala Glu His Gln Met Ile Val Ile Ser
100 105 110

Cys Gly Ser Arg Ala Leu Phe His Cys Arg Phe Tyr Ala Ser Arg Pro
115 120 125

<210> 108

<211> 49

<212> PRT

<213> Chlamydia pneumoniae

<400> 108

Ala Leu Leu Ser Arg Ala Cys Val Ala Ser Ile Ile Pro Ala Arg Lys
1 5 10 15

Ser Ala Ser Ile Ala Ile Cys Leu Pro Gly Ile Ala Ser Asn Arg Asn
20 25 30

Arg Ala Ala Thr Ser Ala Thr Arg Ser Ala Pro Leu Val Thr Thr Ile
35 40 45

Asn

<210> 109

<211> 48

<212> PRT

<213> Chlamydia pneumoniae

<400> 109

Asn Lys Val Ile Thr Gly Ser Trp Arg Val Gly Ala Cys Glu Ser Met
1 5 10 15

Glu Thr Arg Lys Pro Pro Lys Cys Leu Lys Lys Lys Val Asp Arg Glu
20 25 30

Lys Ala Val Asn Ile Glu Thr Ile Lys Val Thr Ala Glu Gly Lys Ser
35 40 45

<210> 110

<211> 116

<212> PRT

<213> Chlamydia pneumoniae

<400> 110

Gly Ile Ser Val Met Met Met Leu Ser Arg Cys Leu Ser Ser Phe Ser
1 5 10 15

Ser Thr Cys Arg Arg Ala Arg Thr Leu Ile Phe Pro Arg Pro Val Val
20 25 30

Tyr Val Glu Arg Ile Pro Ser Glu Pro Gln Ile Ile Pro Pro Val Gly
35 40 45

Lys Ser Gly Pro Gly Met Thr Cys Lys Ile Ser Ser Thr Glu Ala Cys
50 55 60

Gly Phe Ala Ser Arg Arg Ser Val Ala Ser Ile Ser Ser Pro Lys Leu
65 70 75 80

Cys Gly Gly Ile Phe Val Ala Ile Pro Thr Ala Ile Pro Glu Glu Pro
85 90 95

Leu Gln Arg Arg Phe Gly Asn Leu Glu Gly Lys Thr Thr Gly Ser Cys
100 105 110

Phe Val Ser Ser
115

<210> 111

<211> 148

<212> PRT

<213> Chlamydia pneumoniae

<400> 111

Ser Gly Arg Ile Ile Ser Val Met Leu Ser Ala Pro Pro Cys Glu Leu
1 5 10 15

His Ser Asp Leu Ile Asp Pro Asp Leu Phe Glu Phe Asn His Arg Leu
20 25 30

Asn Ile Cys Ile Ser Ala Glu Val Arg Gly Arg Val Thr Thr His Thr
35 40 45

Phe Arg Gly Asp Ser Cys Asn Met Ser Phe Asn Cys Ser Val Arg Gly
50 55 60

Asn Val Ile Thr Ile Pro Arg Ile Ile Arg Ile Glu Ile Arg Ser Leu
65   70   75   80

Thr Ser Ser Phe Ser Ile Ile Thr Lys Cys Lys Arg Ile Ser Ser Arg
                85   90   95

Leu Arg Ile Thr Asn Ile Ile Ala Tyr Trp Ser Leu Arg Tyr Val Cys
            100   105   110

Leu Arg Ile Asp Ile Lys Thr Val Arg Glu Cys Ser Ser Ile Lys Leu
        115   120   125

Arg Thr Phe Arg Arg His Ile Thr Leu His Asn Lys Phe Thr Trp Arg
    130   135   140

Ser Arg Gly Ile
145

<210> 112

<211> 60

<212> PRT

<213> Chlamydia pneumoniae

<400> 112

Ser Asp Arg Asn Ser Phe Ser Ile Ser Val Ser Phe Ser Lys Tyr Ala
1   5   10   15

Asp Phe Ile Ala Pro Leu Asn Trp Ser Leu Arg Thr Arg Arg Ala Phe
            20   25   30

Asn Pro Val Glu Ala Ala Leu Ile Arg Phe Ser His Ser Ser Arg Val
        35   40   45

Arg Pro Glu Val Thr Val Pro Glu Ile Arg Asn Ser
    50   55   60

<210> 113

<211> 63

<212> PRT

<213> Chlamydia pneumoniae

<400> 113

Met Pro Trp Ile Phe Tyr Lys Leu Phe Asn Ile Asn Ile Gly Val Ile
1   5   10   15

Lys Thr Gly Phe Gly Phe Cys Thr Cys Gly Arg Lys Arg Ser Ile Glu
20 25 30

Phe Val Leu Phe Phe Asn Asn Thr Asn Ser Ser Ser Pro Thr Ser Ser
35 40 45

Asn Gly Phe Asn Asn Asn Arg Glu Thr Tyr Phe Phe Ser Tyr Phe
50 55 60

<210> 114

<211> 85

<212> PRT

<213> Chlamydia pneumoniae

<400> 114

Ile Ser Met Ser Ser Ile Glu Thr Pro Ser Ser Pro Thr Thr Ser Ile
1 5 10 15

Arg Leu Pro Ile Ser Glu Pro Phe Ser Arg Asn Cys Ala Ala Phe Phe
20 25 30

Thr Ala Pro Pro Gln Pro Glu Thr Phe Ser Ser Lys Ile Cys Pro Thr
35 40 45

Trp Phe Lys Tyr Phe Asp Gln Glu Ile Lys Gly Ser Ile Glu Gly Tyr
50 55 60

Leu Arg Ala Ser Ala Arg Ala Phe Glu Arg Pro Gln Asn Ala Pro Thr
65 70 75 80

Thr Ala Asn Val Asp
85

<210> 115

<211> 45

<212> PRT

<213> Chlamydia pneumoniae

<400> 115

Gly Asp Leu Glu His Tyr Lys His Ile His Gly Pro Phe Ser Lys Ser
1 5 10 15

Ser His His Gly Lys Arg His Lys Arg His Asn Tyr Leu Met Phe Leu
20 25 30

Gln Cys Arg Tyr Lys Thr Leu Cys Gly Asp Gln Glu Ser
35 40 45

<210> 116

<211> 29

<212> PRT

<213> Chlamydia pneumoniae

<400> 116

Arg Val Ser Phe Asn Ala Ser Pro Pro Ile Thr Thr Ser Arg Arg Asp
1 5 10 15

Ser Lys Gln Glu Phe Cys Phe Phe Ala Val Phe Arg Ile
20 25

<210> 117

<211> 86

<212> PRT

<213> Chlamydia pneumoniae

<400> 117

Ser Ile Asn Pro Leu Ala Pro Gln Arg Ser Leu Gly Pro Ala Ile Gln
1 5 10 15

Tyr Gln Leu Glu Glu Trp Pro Ile Gln Asp Thr Ser Ile Ser Arg Asp
20 25 30

Pro Lys Arg Leu Ser Ser Thr Asn Thr Ser Val Ser Tyr Arg Asn Ala
35 40 45

Ser Glu Ile Phe Ser Cys Asn Ser Ser Leu Ser Arg Thr Lys Asn Ile
50 55 60

Pro Ile Leu Asp Pro Lys Cys Ala Val Phe Thr Ile Ile Gly Lys Glu
65 70 75 80

Asn Val Ser Ile Arg Phe
85

<210> 118

<211> 45

<212> PRT

<213> Chlamydia pneumoniae

<400> 118

Pro Leu Gly Pro Ala Pro Ile Thr Thr Gln Ser Asn Ser Trp Val Ile
1 5 10 15

Phe Ser Leu Thr Val Ile Lys Ile Ser Lys Arg Thr Pro Leu His Lys
20 25 30

Cys Met His Leu Ile Lys Lys Arg Thr Leu Cys Leu Phe
35 40 45

<210> 119

<211> 69

<212> PRT

<213> Chlamydia pneumoniae

<400> 119

Gly Glu Gln Pro Phe Leu Phe His Pro Thr Ser Gln Gln Ser Leu Ser
1 5 10 15

Leu Tyr His His Tyr Ile Gly Thr Leu Gln Ser Ser Phe His His Trp
20 25 30

Lys His Pro Leu Gln Lys Ile Ala Phe Pro Gln Lys Ile Phe Gln Asp
35 40 45

Gln Gln Val His Arg Leu Pro Thr Ser Gln Arg Gly Lys Thr Asp Leu
50 55 60

Asp Pro Arg Phe Leu
65

<210> 120

<211> 95

<212> PRT

<213> Chlamydia pneumoniae

<400> 120

Val Thr Ser Lys Tyr Ala Ser Met Arg Pro Ser Ile Pro Asn Pro Ala
1 5 10 15

Ser His Thr Arg Lys Ile Ala Arg Ala Pro Thr Ser Arg Leu Thr Arg
20 25 30

Phe Pro Tyr Ala Gly Tyr Ile Ser Ser Lys Lys Tyr Gln Gly Ala Pro
35 40 45

Val Ser Pro Gln Gly Arg Ser Glu Pro Ser Gly Asn Thr Met Arg Phe
50 55 60

Glu Glu Ser Pro Gly Thr His Thr Arg Pro Pro Ser Pro Arg Thr Asp
65 70 75 80

Ser Glu Ile Asn Arg Ser Leu Ser Leu Pro Gly Ile Ala Val Gly
85 90 95

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